GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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July 30, 2004, 14:16:25; Search time 3640 Seconds (without alignments) 7251.623 Million cell updates/sec
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Perfect score:
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6: gb_pt:*

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11: gb_ph:*

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25: em_ph:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RS Wing, R.A., Yu.Y. Soderlund, C., Kim, H., Rambo, T., Saski, C., Currie, J., Collura, K., Minx, P., Du, H. and Thurmond, S.K. Direct Submission

AL Submitted (17-287-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA

Arizona, AZ 802 Forbes, AZ 85721, USA

A sequence was finished as forberwise notes in lecrate channed by many are second by high quality data (i.e., phred quality as compressions and the assembly was confirmed by restriction as compressions and the assembly was confirmed by restriction digest. The following areas contain TA randem repeats: 5185-5280 (124-48 pairs), 6500-6589 (11-45 pairs), 11108-11153 (23 pairs), 11895-1139033 (39 pairs) and 138799-139886 (19-44 pairs). There are bacterial transposons at these locations: 5705-7578, 1974-5735, 1917-93354, 97860-100004, 118324-18868 found in these locations are below threshold: 30629-306668 and 102644-102651. Every attempt has been made to resolve these areas and future attempts will be made as new techniques arise. There is only overlap covering 120649-120552 and 141891-141908. The mucleotide sequence of this BAC clone was generated by combining Monsanto, Syngence and Arizona Genomics Innellegues equencing date areas made are sequenced and Arizona Genomics Innellegues esquenced area. The assembly overlaps from base 11590-15510 with OSANBA0013071

Caccession #ACO79843). The overlap is from base 1-40920 on
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YMCDPADGVRENWPDSGEDVHGHIIGYGFWGFYCWYKWHGEGEGGGGAAANRSGAHN
YMCDRADGVRENWPOSGEDVHGHIIGYGFWGFADVEDPAQNERDGKESRLYSDSETPL
YAGCKAKHTKLSYILDDMKLKASSGWTDKSFTDLLGILKAMLPVENTLPEMTYGAKQV
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GCNGKKSLISHVCNDERIBSYFSSILYINGDSGSGSIAHAKKRMERILTUREKFTDI
DENDWYNPYSTVSQMTGGSKVVIISRIENLARFCTAKAVHLNSLSQEEYSYLFKMLA
TDQXDHPKMVSVANDLAVVLGGSLIIANMISDMLRRNHNVHFWLRILRRFERMVKNNF°
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/mol_type="genomic DRA"
/sub_species="(japonica cultivar-group)"
/db_tref="taxon:3947"
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/note="Mypothetical protein"
complement(join(2435 . .2524,2625 . .3620))
/gene="OSJNBb0004A06.2"
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/note="Simple Sequence Repeat (TA)n"
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/protein_id="AAN11186.1"
/db_xref="GI:22953953"
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/db_xref="GI:22953952"
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Oryza sativa (japonica cultivar-group)
Bukaryota, Virdiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Submitted (19-NOV-2001) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA

3 (Dasses 1 to 153310)

S Wing,RA. Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T., Saski,C., Henry,D., Oates,R. and Simmons,J.

Direct Submission

I. Submitted (25-AFR-2002) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA

4 (Dasses 1 to 153310)

S Wing,RA. Yu,Y. Soderlund,C., Kim,H.-R., Rambo,T., Saski,C., Currie, J. and Collura,K. Soderlund,C., Kim,H.-R., Rambo,T., Saski,C., Submitted (28-ARG-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, A2 85721, USA

S Wing,RA. Yu,Y., Soderlund,C., Kim,H., Rambo,T., Saski,C., Currie,J., Collura,K. and Thurmond,S.K. Rambo,T., Saski,C., Currie,J., Collura,K. and Thurmond,S.K.
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Ming, R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T.,
Saski,C., Henry,D., Oates,R. and Simmons,J.
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OSJNBD0004406, complete sequence.
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Gaps

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Direct Submission The Institute for Genomic Research, 9712 Submitted (05-MY-2003) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850. USA This is the pseudomolecule for rice chromosome 10, which was constructed by resolving discrepancies between overlapping BACs, trimming the overlap regions, and linking the unique sequences to form a configure sequence. Genes in individual BAC clone were identified by a combination of several methods: Gene prediction programs searches of the complete sequence against a peptide database and EST databases. Genes without significant peptide similarity but with EST similarity are named as unknown prodeints Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding ENNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wistl.edu/eddy/tRNAscan-SE/).
TLVYDLWTFGPRREIASSIAELKVRAQLIADRRIRYGVENPNTQKGKGPPDATSYDIA
BOLASHELGKNBFVGMEKANCDLERWFOGTAGEPRIVSI 1VGFGGVGKTTIANALYK
KVWYQFDCRAWYTSONYDLDAVLADILKQIDPDYRQQCSSKTGTSBNIKTLARFGSK
KKRDVQRTGSLRQSSPRSIBETSNLKRIETTDNKLESQIKKLLDKKRCVHPSIHLSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group) chromosome 10, section 7 of AEO17053 AEO16959
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/note="Chromosome Sequence Derivation: nucleotide sequence
in this region was derived from BAC clone OSJNBD0072F04
(GB.AC092535).
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/locus tag="OSJNBb0072F04.10"
/loces="contains similarity to NPK1 related protein kinase"
complement (<6121. .>7701)
/locus tag="OSJNBb0072F04.10"
complement (6121. .7701)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryseae; Oryza.
1 (bases 1 to 303511)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 303511)
Buell, C.R., Wing, R.A., McCombie, W.R., Messing, J. and Yuan, Q.
Direct Submission
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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="genomic DNA"
/cultivar="Nipponbare"
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0
                                                                                                                                                                                                                                                                  3.4%; Score 21; DB 8; Length 153510;
100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indels 0
                                                                                                                                                   26913. .27062
/note="Similar to Tourist_Oll MITE element"
complement(27190. .27338)
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/chromosome="10"
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                                                                                                                                                                                                                                                                                                                                    Matches 21, Conservative
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BEDRQTAQINDLLVRDLKDSTEGLKVIIDHTFTS"
complement (24383. .25405)
//note="Colubno004406.5"
//note="Contains similarity to disease resistance protein"
complement (24383. .25405)
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IQVLDFQGLKGFKNRHMKHICKMFVLKYLSLRGTDITHVPPTIVKLSYLBTLDIRETR
VKELPKEVEQELKISRILGGSKNKNPRKGLRLPQEKSKKKQKGKSMLTQDKEKEGNKAL
RISGIKIDETTAVAGLHQLTGLKKLITYKLKLNPEPGTRKIHTELRSSIEYLCSCG
LQTLAINBEGGSNRINSLGANSAPPRYLVALELSGMLKKPPGMIKTLRTLSKTILSLIL
VLRTDTLEHLRALPLFSFSFGEMEKDQDKKMKDIIEDNKSLSDGEIFVPGEGFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trānslation="MNLNNVGKKGLITDHANMKKÇKRKKEKGNRSDWHGSTKDTIPFM
GDADFNHAPEFGVYDGYACGTYQMAPALLLLCFHQQLWQIQSKCCYYTSSASSTGGGR
GQAAWAWYAIWFPADKGGTAAADEBGGWLLRIARQRGADRQRWKGSRWRPWAEERQ
APFVVBLASRSRRRADGLSPVPTTRSSYSLLITGQBALMQBYRGKVSAWYTESRSLIGS
SLARIQAESFCSGRNRNGKGSIKFILRIKDLFVDESHELFLNRHDKFLVCEASKSKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQWNLQCSSIKCNIETIWPWGGISLHLLQNRQDVIFRRDFRGRKNYIIVILILRRSG
ICIGALKEIPKPPIFKHERSFRPPVLRIENGNDGSMITLQHGQVINSGIWIIKTPFH
CKTSVQPFQNQILTILLLIGPSGPSEAFLDMEESNKNSIVEKFRQHFSSPQFKNIQBQ
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SLAILDGVTRILDCCYNNLPGYLRTCLLYLAIPPKGWKISRKCLSRRWIAEGFVNAKQG
LTABEVAESYFNHILRRKLIRPVEHSSNGKLKTFQVHDMVLDYIVTKAREENFITVVG
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ASMKAFLLDLAREDPDNRKKHWMKQIRDMAYDCEDCIDDFAHRLPNDSLDAKCCPWIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŻKQQERGSCITŚQSIMPKLDWKKASEKALTLACCSTVQGPPSQAVHTTTASKQCEKÖDK
EPIMQSTPEVGTEEMLVHGSTVKKKLVSSTIEDHVSCNSKNVNTVGKVHQMEPIQSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'translation="MGRGGTEGRSSGAGSGHPRAPVAGGKEREEEVASGLPTLSLPVE"
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RSRIIVTSRPQAVGSTCCRPENKDLLYPISFLSPRDSKELFNRSVSESKSTKDRHKVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /notes="Simple Sequence Repeat (AT)n"
10975. 11020
/notes="Simple Sequence Repeat (AT)n"
complement(19377. .22551)
/gene="OSJNBb0004A06.4"
/notes="Contains similarity to disease resistance protein"
complement(03077. .21480,22331. .22551))
                                                                                                                                                                                                                                                                                                                                                                                                                         "note="Unknown protein"
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loin(8249. .8785/9076. .12789,13220. .13423,14642. .15154)
'gene="OSJNBb0004A06.3"
'note="Similar to Oryza sativa gene, repeat sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="Putative disease resistance protein"
protein id="AAN11188.1"
db_xref="G1:22953955"
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                                                                                                            5542. 5575 Frame Repeat (AT)n" 5502. 5527 //Octe="Simple Sequence Repeat (AT)n" //Octe="Simple Sequence Repeat (AT)n"
                                                                                                                                                                                                                                                                                                   6368. .6457
/note="Simple Sequence Repeat (TA)n"
8249. .15154
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/note="Simple Sequence Repeat (AT)n"
10560. .10589
                                                           .5539
note="Simple Sequence Repeat (AT)n"
                                                                                                                                                                                                                                        5724. .574§
/note="Simple Sequence Repeat
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/db_xref="GI:22953954"
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db_xref="GI:22953956"
                                                                                                                                                                                                                                                                                                                                                                                               gene="OSJNBb0004A06.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVHRVSPSASAHQNRFLT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                             Micropan-1
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/Jocus tag="OSGNBb0072F04.15"
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/note="contains similarity to copia type pol polyprotein"
complement(join(<25322. .26796,27148. .27678,27724. .27814,
28119. .28279,28375, .28542.29526. .>29537))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGDASTSVVLATCLVKVHCKKTGSKVFDSCGDSVLIISRYGRVFKADFENPVSPVITC
LAAKFDKDVMFWHRRLGHVGFDHLTRLSGLDLVRGLPKLKKNIDLDEAFQHFRGLFLR
LDLEFPGSLKRIRSDNGGLEHEFSSPRVPQQNGVVERKYRVLVEMARMMLDEYKTPKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FWARRINTACYISNRVFLRSKLGKTSVELRFGRQPKVSHLRVLSCKCFVLKSGNLDKR
BARSTDGLFLGYPAHSRGYRVLLLETNKIIETCEVSFDBASPGTRPDIAGTLSGVQGG
DGRIFBDBSEDDNNDEVGSAELENFERNKVWTFVEPPSEHNIFGTKWVFKNKQNBDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVRNKTRLVAQGETQVEGLDFDETFAHVARVEAIRLLLAFAISKGFKLYQMDVKSDFL
NGFIQEVYVKQPPGFENPEPPNHVFKLSKALYGLKQAPRAMYDRFKNFLLAKGFSMG
KVDKTLFVLKHGDNQLFVQIYVDDIIFGCSTHALVVEFABTMRREFEMSMMGELSYFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLQIKQTPQGTFVHQWKYTKDLLRRFKMENCKPISTPIGFTAVLDPDEDGEAVDQKEY
RSMIGSLLYLIASRLDIQLAMCLYTRFPASSPRASHRQAIKRIMKYLMHTLEFGIWYST
SSSICLGKYSDTDFGGCRIDKENSGICHFLGTSLIAMSRKOSSVAQSTSSESYVAA
ASCCGGLLMLLSTLKYSLYFEKYDLFCDNTSAINIAKNPVQHSRTHHINICFHFLRD
HVEKGDVELQFLQKMLQLADIFNKPLDSNHFAFLRGELGIIHPFGMV"
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SLPPRQKTPNQPQPSQKSPSTDPIRKKTPTPSASQKGGSSGNERLPHSKSKLVPNPTT
SLPKKYGSSTITSLLGPKKPERRIPIPKVIEHTKCAQPRLPPKPISDFRTLEKSE
MOSSSRELFLDKKASDZBAAFCKSVDLKSLDDIDNLDKABVLLSSNNDDPWRCSYQCRS
LDRKTAFLDPRAVNPNNQLSKEKEIDDYLFNALVKQNGYDHILLPYLSHHHWILFVIN
                                                                                                                                                                                                              complement (join (25322. '26796,27148. '27678,27724. .27814, 28019. .28279,28375. '28542,29526. .29537)}
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YRQPALTNLCGMYVMWYMLCFVESGHLLPRNAEKLGLETSSMLPHVFTALTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSYKALVARKENVWIVDSGYSRHMTGDKNWFSSLKKASKTESII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="contains similarity to NBS LRR type resistance
                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="putative transposase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (<48333. ,>52859)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . >42847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <32428.
                                                                                           mRNA
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                                                                                                                                                                                                                        /translation="yaaaliggggwtrlrsygrgasgavyslaandyggelfylksag
egaarqqlrrewsymsglssphylkclgfyQasggcggehqlfleyapggsladyva
rnggrldbgavrtyaadylrgldylhgklyvhgdykgsnylygadgrakltdfgcary
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/note="contains similarity to NFK1 related protein kinase"
complement (<10528. .>12105)
/locus tag="OSJNBD0072F04.11"
complement (10528. .12105)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAADDNSIRLPRKVGRTASSLPLRYAAPQLLHWPDDAAAVQLRLCAHGRHLVLYVSWA
RCSMPREWLDTYWVCLDALAAAALLGGALDDTARALRRDARLAALWGALADRLCRRVU
VDVCARNGYTLEPTFWSLPDDVKAAILARLPDGDDLARAECTCAGLRRLVADRDRDAA
                                                                                                                                                                                                                                                                                                                                                          AMPGGSKOPVLGGTPAFMAPEVARGEBOGLAADVWALGCTVIEMATGRAPWSDMDNVL
PALHKIGYTDAVPDLPRMLSPEAKDFLRGCLORRAGDRPTAAQLLOHPFISKSCGLNN
KETVKATWVSPTSALDATLWESESSSTDGEEVDDMSSNSPTGRIRAMACSCQTLPDMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDDHGCSWIEVLGSVSINVANKTAAIEQRVTSMACSPSSVPDWDSGNQGWIDVLSSVS
ISIANKLETATAADNVSSECPAKWVRAMACSPSSVPDWDSDQGWIDVLGASPDVVAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFDVAAAADQISGQAVGSIVVGVGSSEQSVVVENQEDBFTSLSSCSERVLLVGVHAAD
NNAASRKAGIKRCSNFSC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLKKEVVKATWVSPTSALDAAALWESTTSSTDDBEADDWSNSPTGRIIAMASSGGG
TLPDWDSDDHGWIEVLGTVSINIAKKKTAAAEDYEASESPAKRVRAMACSFSSVPDWD
SDNHGWIDVLSASPADDNGGEGNAPEEFDVVAAADQIFGEAVGSIVVGVGSEQSVVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tränslation="MADTSPLHKIIGAAWWARPLIGKLVILAHAAFLDAGFVSTGAA
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VVFVCVRRANDHJTYNICLDAPAAAALLAGGLDDTRALARRERGAKLAALMSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRLCRRVIYDLCARNGYPVEPEHELMSLPDDVKVA LLARLAAGEDLARVECTCVGLNI
LVAEHDSTLWKPMYTKLRSQLRRRLRFLGVSYGEPTAVSWKARYVAVRRRRVPAAHDV
FMGELLLPVMTEWMRVPWIRRYPFVPPPPFESPEEBETVVPRRRRRRAMPRDAGHGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NQEDEFISLSYCSERILLVAVHAADNNAASRKAGIKECSHDPRPSIPSRCAHNLFLSL
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DDVLAALRMIGYTDAVPDLPPWLSPEAKDFLRRCMQRRAGDRPTAAQLLQHPFVSKSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MAKPKTSPLHRVIGAARWDAERPLGRLLILAHAAFLDAGFVPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LWKPRYEKLPFLLQLIGGGDDDGEPTTEVSWKKKYVAARLWPFGELFASMRETRRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IYAPLLDLDFDSFTRFWVFDDKPSPLPEEITVPRHRRRRRRRAMPRDAGHGLAARGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVVARNGDRLDESAFRAYAADVLRGLDYLHEKLVVHGDVKGSNVLVGADGRAKLADFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative NPK1-related protein kinase" /protein_id="AAP51983.1" | db_xref="GI:31430012"
                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAPGHGGDKKQWRGAGAVHSPSSGFRWKHR"
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<16098. .>17177
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/locus tag="OSJNBb0072F04.12"
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/note="unknown_protein"
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19076. .20170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                                                                                                      rotein_id="AAP51982.1"
o xref="GI:31430011"
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SOURCE

Db

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/GONTANTILSGLAFRGGTRKNDTNNTMQTIVSRMSEQEMQAVSEYIATLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus tag="NE0273"
/note="Signal predicted by SignalP 2.0 HVM (Signal peptide
probabilty 1.000) with cleavage site probability 0.999 at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="wrkfsvflllanifvvfylhgrpddnlpaqialihsexiellpa
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VLBQFEFDIRNPTEQITESVRQLAQQFPETKLEVTECSRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2595. .2660
Jacous_eag="NE0274"
/note="61gnal predicted by SignalP 2.0 HWM (Signal peptide
probabilty_0.892) with cleavage site probability 0.890 at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function="InterPro IPR000345:IPR002329:IPR003088 COGs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function="InterPro IPR000994:IPR001714:IPR002467 COGs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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transl_table=11
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                                                                                                                                                                                                                                                                                                                      experimental
                                                                                                  complement (1253. .1660)
locus tag="NBD272"
complement (1253. .1660)
locus tag="NBD272"
function="COGS COG3293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein_id="CAD84185.1"
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complement(1853. .2488)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (1853. .2488)
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                                  complement (887. .1698)
   FRFFIHFALIVDHLISVNRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2595. 3197
/locus_tag="NE0274"
2595. 3197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    locus tag="NE0275"
311. .4129
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                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
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                                         misc_feature
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OLVLDIGMIPVVPPKANRVSPWEYDVEMYKKRNEVERLEREREREREFERLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chain, P., Lamerdin, J., Larimer, F., Regala, W., Land, M., Hauser, L., Hooper, A., Klotz, M., Norton, J., Sayavedra-Soto, L., Arciero, D., Hommes, N., Whittaker, M. and Arp, D. Complete genome sequence of the ammonia-oxidizing bacterium and obligate chemolithoautotroph Nitrosomonas europaea
                                                                                                                                                                                                                                                                                                                                                                                                                        313050 bp DNA linear BCT 23-APR-2 Nitrosomonas europaea ATCC 19718, complete genome; segment 2/10. BX321857 AL954747
BX321857.1 GI:30138174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales;
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                                                                Query Match 3.4%; Score 21; DB 8; Length 303511; Best Local Similarity 100.0%; Pred. No. 2; Matches 21; Conservative 0; Mismatches 0; Indels 0;
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Nitrosomonas europaea ATCC 19718
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complement (885, .1253)
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1. .313050
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moleculaire, Universite Libre de Bruxelles, laboratoire de Biologie
du Developpement, Rue des chevaux, 67, 1640 Rhode St Genese,
BELGIUM
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ESENVCQERDSDPDKFFAEFIYEYSRRHPDLSTPRLLRITKVYMDFLEDCCSRENPAG
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                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Submitted (15-SEP-1998) Van Reeth T., departement de Biologie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE 522099"
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1. .2680
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                                                                                                                                   linear
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Mus musculus mRNA for alpha-albumin protein.
AJ011080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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Matches 20; Conservative
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MMU011080/c
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AC117443/c
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MNALRLTEGFDPGLFHTRTGLTIASI QKSLAZAEQRGLI EWQHDCIRPTPEGRRFLND
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Eukaryota; Merazas, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2219)

1 (Dases 1 to 2219)

2 Murny, D. M., Adams, C., Adio-Oduola B., Ali-Osman, F.R., Allen, C., Alsbrata, J., Barbaria, J., Bencho, J., Brake, J., Barbaria, J., Dadarez, D., Chon, G., Chen, E., Davete, C., Burrell, K.L., Bydd, M.C., Carron, T. B., Davis, C., Davis, C., Coyle, M.D., Dabaria, C., Davis, C., Coyle, M.D., Dabaria, S., Davis, C., Davis, C., Ederich, D. A., Davis, C., Darger, M., Dugan, Rocha, S., Davis, C., Davis, C., Edar, J., Edar, J., Ederich, D. A., Garcia, M., Garcia, A., Garner, T., Garcia, P., Han, Y., Falls, T., Edar, D., Edwards, C. C., Elbj, C., Escotto, M., Falls, T., Edar, J., Edwards, C., Elbj, C., Escotto, M., Hextrandez, O., Harris, K., Harr, M., Harlak, P., Hale, S., Hume, J., Harrandez, O., Harris, K., Harr, M., Harlak, P., Haves, M., Holloway, C., Harrandez, O., Harris, K., Harris, K., Harrandez, O., Harris, K., Harrandez, O., Harris, K., Harris, K., Harris, K., Harrandez, O., Harris, K., Harris, C., Licuis, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris
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Submitted (26-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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Submitted (10-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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   AC117443.4 GI:22024339
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3 (bases 1 to 22190)
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Worley, K.C.
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                                                            Homo sapiens (human)
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Baylor Plaza, Houston, TX 77030, USA on Jul 31, 2002 this sequence version replaced gi:20335979. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
                                  COMMENT
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 18:34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Exports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="overlaps bases 94715. .96701 of clone AC128685"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(21804. .22190)
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                                                                                                                      /rpt_family="THE1B"
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ement(Ao1
complement (8414. .8473)
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complement(8797, .893
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15969. .16000
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HTG; HTGS PHASE0.
Mus musculus (house mouse)
Mus musculus
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2 (bases 1 to 86385)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,

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Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, P., DeArellano, K., Dewarr, K., Dewarr, K., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Faro, S., Erreira, P., FitzGerald, M., Gage, D., Galagan, J., Gondy, S., Godd, S., Craham, L., Grand-Pierre, N., Hafez, N., Hulme, M., Iliev, I., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Indblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marenga, V., Murphy, T., Naylor, J., Mencus, L., Miloo, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Ratge, K., Sase, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, N., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, N., Talamas, J., Tasjaye, S., Theodore, J., Topham, K., Travers, M., Vassilav, H., Viel, R., Vo, A., Wilson, B., Wu, X., Travers, M., Vassilav, H., Viel, R., Vo, A., Wilson, B., Wu, X., M., Nassilav, H., Vell, R., Vo, A., Wilson, B., Wu, X., Shomission Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:

Smit, A.F. A. Green, P. (1996-1997)

http://cryp.gamem.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This record contains 80 individual
* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
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g of 971 bp in length
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Mus musculus clone RP24-383E18, DNA linear HTG 27-DEC-2002 AC138385,1 GI:27375071
HTG; HTGS PHASE0.
Mus musculus (house mouse)
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Birren, B.; Nusbaum, C. and Lander, E.
Mus musculus, olone RP24-383E18
Unpublished
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Smit, A.F.A. & Green, P. (1995-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matchews, C., McCarthy, M., Meldrim, J., Meneus, L., Minova, T., Mlanga, V., Murphy, T., Maylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Neal, D., Olivez, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Scojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
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Center: Whitehead Institute/ MIT Center for Genome Research
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sequencing reads that have not been assembled into
contigs. Huns of M are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
voverlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ project Information
Center project name: 1.26666
Center clone name: 383_E.18
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STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANNOTATION OF FEATURES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 121201)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases I to 12120)

Nuzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Burata, J., Benton, J., Bimder, W., Bromin, D., Burbaria, J., Benton, J., Binder, M., Brown, M., Bryant, N.P., Burbay, C., Burch, P., Burket, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carron, T.F., Chen, R., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Davida, M., L., Dederich, D., Delaney, K.R., Dalgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Barnilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., He, X., Hernandez, J., Hernandez, J., Huber, J., Huber, J., Hulyk, S., Hume, J., C., Hume, J., C., Hulls, B., Homesi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
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Homo sapiens 3 BAC RPI1-535124 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
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Pred. No. 7.4;
8: contig of 1015 bp in length
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1: gap of 100 bp
0: contig of 993 bp in length
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7: contig of 999 bp in length
7: contig of 984 bp in length
1: gap of 100 bp
9: contig of 958 bp in length
9: gap of 100 bp
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9: contig of 999 bp in length
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9: contig of 997 bp in length
7: contig of 998 bp in length
1: gap of 100 bp
1: gap of 100 bp
1: contig of 996 bp in length
4: contig of 996 bp in length
4: gap of 100 bp
6: contig of 996 bp in length
7: contig of 996 bp in length
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llarity 100.0%; Pr
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Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,

Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,

Kovar, C., Krachovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,

Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,

Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,

Mardinez, E., Massey, E., Maucie, Martindale, A.,

Martinez, E., Massey, E., Mawhiney, E., McLedd, M. P., Meador, M.,

Moore, S., Morgan, M., Moorish, T., Morled, M. P., Meador, K.,

Noore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Nguyen, N.,

Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N.,

Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N.,

Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N.,

Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N.,

Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S.,

Sonaike, T., Sparks, A., Stanley, H., Stone, H., Stuton, A., Svatek, A.,

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Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L.,

Warra, V., Villalann, D., Vinson, R., Wang, S., Ward-Moore, S.,

Williamson, A., Wleczyk, R., Mooden, S., Williams, G., and

Gibbs, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 121201)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (25-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 121201)
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Submitted (26-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 121201)
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Submitted (21-JUN-2003) Human Genome Sequencing Center, Department
Submitted (21-JUN-2003) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, T77030, USA
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                  http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
                                                                                                                                                                                                                                                              QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="overlaps bases 176428. .178521 of clone AC112644"
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/organism="Homo sapiens"
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4169. .4349
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/db_xref="taxon:9606"
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complement(8280. .8524)
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8525. .8671
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2802. .13984
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14730. .15081
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3981. .4016
/rpt_family="(TTTA)n"
complement(4017. .4168
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/rpt_family="AT_rich"
1756. 4789
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5854. .5902
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6406. .6462
/rpt_family="AT_rich"
complement(7193. .8279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-535124"
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/rpt family="L1MA3"
2212. . 3980
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rpt_family="LIMA3"
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4691_
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complement(8672, .10
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complement(10517. .
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2308. .12628
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2629.
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10087.
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Discrete B., Initon, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Birren, B., Initon, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barra, N., Baguslavkil, L., Boukhgalter, B., Brown, A., Camparate, J., Campapiano, A., Choepel, Y., Colangelo, M., Collins, S., Callymore, A., Cooke, P., Dehrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Goyette, M., Grandam, L., Grand-Pierre, N., Gardan, L., Grand-Pierre, N., Gardan, S., Ginde, S., Goyette, M., Grandam, L., Grand-Pierre, N., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, K., Liu, G., Machan, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwah, P., McKernan, K., Marquis, N., Matthews, C., McCarthy, M., McEwah, P., McKernan, K., McPheters R., Melthews, C., McCarthy, M., McEwah, P., McKernan, K., McPheters, M., Molova, T., O'Norman, C., Norman, C.H., O'Connor, T., O'Oonnell, P., O'Neill, D., Oilver, J., Resent, R., Seuery, P., Rouge, R., Schupback, R., Seamens, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Travers, M., Travers, M., Trajallo, J., Young, G., Zainoun, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Cembek, L., Zimmer, A. and Zody, M.
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Homo sapiens chromosome 15 clone RP11-762M18 map 15, WORKING DRAFT SEQUENCE, 8 unordered pieces.
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ACO90177.3 GI:22122959
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Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 154934)
Homo sapiens chomosome 15, clone RP11-762M18
Unpublished
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.0506. .20802
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                                                                                                                                                                                                                                                                                  rpt_family="MER41B"
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16514. 16799
/rpt_family="LIM4"
complement(16812. .)
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complement(18849...)
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Direct Submission

Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 154391)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Canarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Grarde, J., FitzGerald, M., Gage, D., Galagan, J., Garderia, P., FitzGerald, M., Gage, D., Galagan, J., Hane, W., Ilaev, Ilaev, Ilaev, Herren, N., Hagos, B., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, MacLean, C., Macdonald, P., Major, J., Matthews, C., Norman, C., MacLean, C., Macdonald, P., Major, J., Matthews, C., Norman, C., Peterson, R., Phunkhang, P., Pierre, N., Retta, R., Ries, C., Norman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zember, L., Zimmer, A. and Zody, M.

Submitted (6-AUG-2002) Whitehead Institute/MIT Center for Genome Research along Street, Cambridge, MA 02141, USA On Aug 6, 2002 this sequence version replaced gi:1395454.

All repeats were identified using RepeatMasker: html
Center: Whitehead Institute/ MIT Center for Genome Center: Whitehead Institute/ MIT Center for Genome Center: Whitehead Institute/ MIT Center for Genome Center code: WIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site, http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Conter project Information
Center clone name: 112158
Center clone name: 762 M.18
Center clone name: 762 M.18
Sequencing vector: Plasmid; n/s; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 152208 bases at least Q30
Consensus quality: 153208 bases at least Q30
Consensus quality: 153909 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 157000; agarose-fp
Unsert size: 157000; agarose-fp
Unsert size: 157000; agarose-fp
Unsert size: 157000 bases; sum-of-contigs
Quality coverage: 8.6 in Q20 bases; sum-of-contigs
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gap of 100 bp
contig of 53585 bp in length.
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Location/Qualifiers

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A Gardyna, Inition, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N.; Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Colampoplano, A., Chopepl, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyar, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lohos, Y.J., LaRocque, K., Lamazares, R., Landers, T., Laborine, R., Liu, G., Macdenan, C., Macdonald, P., Marquis, N., Mathews, C., Macdenan, C., Macdonald, P., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murph, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C., Norman, C., Murph, T., O'Donnell, P., O'Neil, D., Olliver, J., Retta, R., Ries, C., Rogov, P., Romen, J., Rosetti, M., Ribey, R., Schuback, R., Raise, C., Rogov, P., Romen, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Talamas, J., Tesfaye, S., Theodore, J.,
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Homo sapiens chromosome 15, clone RPI1-797A18, complete sequence.
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1 (bases 1 to 157793)

Birren, B., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 15, clone RP11-797A18
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100.0%; Pred. No. 7.8;
ive 0, Mismatches 0; Indels 0;
                                                                                                                                                                              clone_lib="RPCI-11 Human Male BAC"
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28748. .42560
28748. .42550
42661. .66512
/note="assembly_fragment"
66613. .101249
/note="assembly_fragment"
66613. .101249
101350. .154934
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5051. 5258
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                                                                                /chromosome="15"
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Best Local Similarity 100.0
Matches 20; Conservative
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JOURNAL REFERENCE AUTHORS

TITLE

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Center: Whitehead Institute/ MIT Center for Genome Research
         Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 17, 2003 this sequence version replaced gi:23308099. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                       Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-11 Human Male BAC"
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                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
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2713. 2717
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11743. .1205?
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empart(1.0)
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459. ...469
                                                                                                                                                                                                                                                                                                                                                   Center project name: L12167
Center clone name: 797_A_18
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family="(TA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="L1MB3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="LIMB3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family="AluJo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family="AluSq"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="L1MB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="(TA)r
complement(10024.
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complement(9366.
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complement(10538
                                                                                                                                                                                                                            Center code: WIBR
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12582.
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12054.
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                                          COMMENT
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S. (bases 1 to 157793)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachofli, H. M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachofli, H. M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachofli, H. M., Barna, N., Carag, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorlis, L., Erickson, J., Farco, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, N., Johnson, R., Jones, C., Kamat, A., Kartas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, P., Schupback, R., Sewery, P., Smith, C., Spencer, B., Stange-Thomann, W., Schupback, R., Stanger, P., Schupback, R., Stanger, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                            Birren, B., Nusbaun, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaun, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Chopeal, Y., Collymore, A., Cooke, P., Chang, J., Chazara, B., Dakrellano, K., Dawar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hagos, B., Karates, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., Kanat, A., Mcarthy, M., Meddrim, J., Moneus, L., Mihova, T., Mlenga, V., Mcatthy, M., Meddrim, J., Moneus, L., Mihova, T., Merga, V., Wythor, J., Nguyen, C., Nicoll, R., Norbu, C., Norman, C., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schube, C., Schubback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Zimmer, A. and Zody, M., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Librated (104-007-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA.

Research, 320 Charles Street, Cambridge, MA 02141, USA.

E 4 (bases 1 to 15779)

B 1xran, B., Nusbaun, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguelavkiy, L., Boukhgalter, B., Conck, A., Cooke, P., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., PitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Garnd-Pierre, N., Hafez, N., Hardon, S., Gord, S., Graham, L., Cannes, T., Levine, R., Marcha, A., Kartadas, A., Kartadas, A., Kartadas, M., Kells, C., Landers, T., Levine, R., Michiad-Toh, K., Liu, G., MacClean, C., MacGonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Micol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Stanga, C., Regov, P., Roman, J., Roy, A., Schauer, S., Schubback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomam, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Wwman, D., Young, G., Zainoun, J., Zambek, L., Zimmer, A. and Zody, M. Direct, Submission
Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 157793)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (17-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 5 (bases 1 to 157793)
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* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* The finished sequence as soon as it is available and the accession number will be preserved.

* 2590 contig of 2589 bp in length.

* 2690 171061. contig of 100 bp
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100.0%; Pred. No. 7.9;
tive 0; Mismatches 0; Indels 0;
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HTG: HTGS PHASE2: HTGS_FULITOP; HTGS_ACTIVEFIN.

MAS musculus (house mouse)

MAS musculus (house mouse)

Bukaryota; Matzaca; Chariata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 171061)

Mus musculus chromosome 16, clone RP23-176C2

Anderson, S. marna, N. Bastien, V. Boguslavkiy, L. Boukhgalter, B. Anderson, S. Mastien, V. Chang, V. Chazaro, B.,

Choepel, Y. Colangelo, M. Collins, S. Collymore, A. Cook, A.,

Choepel, Y. Colangelo, M. Collins, S. Collymore, A. Cook, A.,

Choepel, Y. Colangelo, M. Gage, D. Galagan, J. Gardyna, S.,

Ginde, S., Goyette, M., Graham, L., Gandariere, N. Ferreira, P., FitzHugh, W., Ggeb, D., Galagan, C., Macarthy, M.,

Machan, P., McKernan, K., Melle, W., Illev, I., Johnson, R., Jones, C.,

Macdonald, P., Majoro, L., Marquis, N., Mathews, C., Miccl, R., Norbu, C.,

Mardonald, P., Major, Y., Mayon, C., Nicol, R., Norbu, C.,

Norman, C.H., O'Connor, T., O'Donnell, P., Olivier, J.,

Roster, M., Riley, R., Rise, C., Regor, P., Roman, J.,

Roster, M., Ravers, M., Riley, R., Schauer, S., Schupback, R., Sancos, W., Viell, N., Viell, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus chromosome 16 clone RP23-176C2 map 16, *** SEQUENCING AC199266
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complement(13487. .13591)

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                                                                                                                                                                                                                                                                                                                                                                               Birren, B., London, J., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barren, B., Linton, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreiras, P., Fitzhugh, W., Porrest, C., Funke, R., Herena, L., Horton, L., Howland, J.C., Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehcczky, J., Maddonald, P., Marquis, N., McEwan, K., McKernan, K., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nahf, R., Naylor, J., Nilef, M., O'Connor, T., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Va, W., J., Land, J., and Zody, M., Welle, J., Wu, Y., Wyman, D., Ye, W., J., Zhao, J. and Zody, M., Wheeler, J., Wu, Y., Wyman, D., Leither, J., Chan, J., Cha
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Submitted (06-NOV-1998) Whitehead Institute/MIT Center for Genome Submitted (06-NOV-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON NOV 6, 1998 this sequence version replaced gi:3845400.
All repeats were identified using RepeatMasKer: Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html.
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      sapiens chromosome 17, clone hRPK.998 F.B, complete sequence.
                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 175066)
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                                                                  AC005900.1 GI:3849824
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                                                                                                                           Homo sapiens (human)
Homo sapiens
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutelecstoni, Metazoa; Chordata; Craniata; Vertebrata; Eutelecstoni, Bulbara; Colon Revalishi, Bulbara; Rodenita; Sciurognathi; Muridae, Murinae; Mus. 18. 10. 1801.2)

All Upublished and Colon Revalishi.

Birran, B. Lintoni, L. Misbuum, C., Landar, E., Ali, A., Allen, N., Anderson, S., Barrana, M. Bartana, V., Gango, D., Galagana, J., Codde, S., Colymor, P., Sepulashi, N., Chara, J. Chases I. to lange, J. Colonge, C., Colline, S., Collymore, A., Camareta, J., Compopiano, A., Colline, S., Collymore, A., Camareta, J., Compopiano, A., Candor, S., Corta, P., Colline, S., Collymore, S., Ferrala, P., Fitzbulh, W., Cage, D., Galagan, J., Godde, S., Gord, S., Goytete, M., Miscoll, M., Machana, M., Liley, I., Colline, S., Collymore, C., Landara, P., Landara, A., Machana, M., Machana, C., Machana, M., Machana, C., Machana, C., Machana, C., Collymor, C., Machana, C., Collymor, C., Machana, C., Collymor, C., Collymor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
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Mus musculus clone RP24-15911, WORKING DRAFT SEQUENCE, 6 ordered
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AC115834
AC115834.
GI:32567880
HTG: HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
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Pred. No. 7.9;
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complement (31788, .32098)

/rpt_family="Ally"

complement (31789, .32098)

/rpt_family="Ally"

/rpt_family="L1883"

complement (32274, .32462)

/rpt_family="MRPR5"
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100.0%; Pred. No. ...
/rpt_family="rigger2"
24517 ...24634
24663 ...25126
/rpt_family="rigger2"
complement(152555...25430)
rpt_family="minger2"
complement(152555...25430)
/rpt_family="minger2"
complement(152555...25627)
/rpt_family="minger2"
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/rpt_family="minger2"
/rpt_family="minger2"
                                                                                                                                                                                                                                                                                   / rpc_family="rigger2"
complement (26829; .26951)
/rpc_family="purine-rich"
complement (26829; .26951)
/rpc_family="purine-rich"
/rpc_family="purine-rich"
/rpc_family="purine-rich"
/rpc_family="purine-rich"
/rpc_family="(CGTT)n"
/rpc_family="(CGTT)n"
/rpc_family="(GGAT)n"
/rpc_family="(GGAT)n"
/rpc_family="(GGAT)n"
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/rpc_family="(GAT)n"
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complement (29470.29778)
/rpt_family="AluSg1"
30002.30029
/rpt_family="AT_rich"
complement (31018.31069)
31070.31140
/rpt_family="LMB3"
31070.31140
/rpt_family="LMB3"
/rpt_family="(Th)n"
complement (31148.31164)
/rpt_family="LMB3"
complement (31148.31164)
/rpt_family="LMB3"
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complement(35003, .35313)
/rpt_family="AluYaS"
/rpt_family="AluYaS"
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ement(32007
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complement(31463.
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DEFINITION

RESULT 14 AC115834 LOCUS

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ACCESSION VERSION KEYWORDS SOURCE

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Cambridgeshire, CB10 15A, WIX. B-mail enquiries:
Cambridgeshire, CB10 15A, WIX. B-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 22, 1999 this sequence version replaced gi:3927920.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: BBBL; SW: SWISSROT; Tr: TREMBL; Wp:, WORMPEP; Information
on the WORWPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 hutp://www.sanger.ac.uk/HGP/Chr22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RP5-1042X10 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                    Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VECTOR: DCYPAC2
IMPORTANT: This sequence is not the entire insert of clone
RPS-1042K10 It may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RPS-1042K10 is at 1 in this sequence.
The true left end of clone RP4-591N18 is at 184081 in this
sequence. The true right end of clone RP3-377F16 is at 39440 in
this sequence.
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hotte="Aludy repeat: matches 140. .312 of consensus"
complement(1419. .1459)
/note="MIR repeat: matches 32. .71 of consensus"
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/note="AluS repeat: matches 276. .298 of consensus"
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note="AluY repeat: matches 1. .309 of consensus"
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    Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: humquery@sanger.ac.uk
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/chromosome="22"
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/clone_lib="RPCI-5"
1. .68
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                                            (bases 1 to 184180)
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                                                                                Beasley, H.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct 8 given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be preserved.

* This conting of 704 bp in length 1501 conting of 100 bp 1
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0
Consensus quality: 178697 bases at least Q30 Consensus quality: 179011 bases at least Q20 Insert size: 176609, agarose-fp Insert size: 179672; sum-of-contigs Quality coverage: 11.4 in Q20 bases; agarose-fp Quality coverage: 11.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 2; Length 180172;
Pred. No. 7.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-24 Male Mouse BAC"
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3.3%; Score 20; ub.
Best Local Similarity 100.0%; Pred. No. 7.9
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176332. .180172
/note="assembly_fragment
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/note="assembly_fragment"
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/note="assembly_fragment"
119608, 176231
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .180172
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LOCUS
DEFINITION
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VERSION
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6143. .7010
/note="Charlie2a repeat: matches 1445. .2313 of consensus"
                                                                                                                                                                                                                                                                                                                                                                        copies 18 mer TCTCTTTCTCTTTC 51% conserved"
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                                                                                                                               repeat: matches 3242. .3313 of consensus'
            'note="AluSx repeat: matches 3. .287 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8918. .8931
/hote="1.5 copies 4 mer AAAT 28% conserved"
8932. .9216
/hote="AluSx repeat: matches 1. .287 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8239. 8547
/note="Alux repeat: matches 1. .309 of consensus"
8856. 8865
/note="2.0 copies 5 mer ATTTC 20% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              copies 9 mer TTTCGCTTT 35% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                 copies 8 mer TTCTTTCC 34% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  copies 8 mer TCCAGCTC 34% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       copies 7 mer TCTTTTT 24% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               copies 7 mer CCACCCT 30% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ... courserved ... 9815. 1 copies 6 mer CTCATT 24% conserved ... fnote="2.1 copies 0 --
                                                                                                                                                                                                                                                  copies 6 mer CTTTCT 39% conserved"
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11602. 11616 copies 6 mer GCCCCA 30% conserved"
//omplement(11986. 12473)
                                                                                                                                                                                                                                                                                                              .5 copies 4 mer TTTC 30% conserved"
                                                                                                                                     ..... of co
..... 8085
/note="4.0 copies 4 mer CTTG 22% conserved"
/note="4.0 copies 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8137. .8151
/note="3.8 copies 4 mer CTTT 23% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   copies 3 mer TAA 20% conserved"
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/note="2.4 cc
8127. .8147
/note="3.0 cc
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/note="3.3 co
                                                                                                                                                                                                                                                                                                                                           8071. .8151
/note="4.5 c
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note="3.3 c
                                                                                                                                                                                                                                                                                  8065. .811
/note="12.
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/note="2.
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product="duli42kl0.4" (novel protein)"
protein_id="CAA12263.1"
db_xref="g1:4176443"
translation="RKISQAVRQQQEQQARMUSALQQQQQQQQQQQQQQQMH8PSHPVG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKPHLDNMVDNALNVGLPDLQYKGPI PGYGSGFSSGGMYGWYGGKEAGTESERKQWT
SMMEGLPSVATQBANNHKNGAI VAPGKTRGGSPYNQPDI I PGDTLGGHTGPAGDSWLP
SMKFGLPSVATQBANNHKNGAI VAPGKTRGGSPYNQPDI I PGDTLGGHTGPAGDSWLP
TDHGLLSRSKSSNASWPPESPGAWPYSASDNSFTNVHSTSAKFPDYKSTWSPDFI
GHNPTHLSNKWMKNHI SSRNTTPLPRPPPGLINKFPSSSWSSTRARSYRGWGTODSKL
ASASTWSDGGSVRPSYMLVLHNLTPQIDGSTLRTI CMQHGPLLTFHLNLTQGTALLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2658. .2868

Chote="11.0 copies 1 mer T 22% conserved"

Tals. .3176

Chote="7.3 copies 3 mer GCA 35% conserved"

Join(3190. .3233,3378. .3561,10740. .10877,13045. .13221,

Join(3190. .3234,3378. .3561,10740. .10877,13045. .13221,

Gene="401042710"

Jene="401042710"

Jene="401042710
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natch: ESTs: Em:AA615306 Em:AA065323 Em:W80019 Em:N75651
Em:AA747718 Em:AA354286"
                                                                                                                                                                                                                                                                        note="L1ME4a repeat: matches 5973. .6118 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       814. .3825
note="6.0 copies 2 mer TG 24% conserved"
complement(3826. .3970)
note="LiMB4 repeat: matches 5746. .5893 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   581. .4879
note="AluSg repeat: matches 1. .299 of consensus"
986. .5106
note="Charlie2 repeat: matches 34. .149 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ote="MER46A repeat: matches 149. .167 of consensus"
                                                                                         note="FLAM_C repeat: matches 1. .132 of consensus"
                                   .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      999. .4074
note="MBR46A repeat: matches 1. .82 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1401. .3425
/note=18.3 copies 3 mer GCA 50% conserved"
complement (3607. .3810)
/note="Mir repeat: matches 19. .226 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                  conserved"
                                                                                                                                                                                                                                                                                                  648. .2666
note="3.8 copies 5 mer CTTT 31% conserved"
                                                                                                                                                                                                                                                                                                                                                           649. 2676

106e="28.0 copies 1 mer T 20% conserved"

650. -2665

note="4.0 copies 4 mer TTIC 23% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="5.3 copies 3 mer CTT 32% conserved" omplement (5266. .5553)
                                                                                                                                                                            335. .2345
note="2.2 copies 5 mer TGTTT 22%
omplement(2420. .2548)
complement (1469. .1766)
/note="AluSp repeat: matches 1.
complement (1786. .1903)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                901. .4459
gene="dJ1042K10.4"
note="match: GSS: Em:AQ549653"
omplement(3974. .3998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 885. .4574
gene="dJ1042K10.4"
note="match: GSS: Em:AQ627708"
                                                                                                                     967. .2589 
note="match: GSS: Em:B14103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3318. .>23457)
gene="dJ1042K10.4"
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Post-processing: Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aaa65395 Brevibact	Aaa65394 Brevibact	Aaa65393 Brevibact	Aca21027 Prokaryot	Ada29053 DNA encod	Aas22742 Human cDN	Aas22506 Human cDN	Ach25483 Human adu	Ach28170 Human adu	Abn92747 Staphyloc	Abl26531 Drosophil	Ada00895 Mouse ost	0	Abl21028 Drosophil	Abn35170 Human spl	Adc90379 E. faeciu	Aah65860 C glutami	Aah34551 Human col	Abx43841 Bovine ES	Abk74808 Bacillus	Aah65859 C glutami	Aca00221 C. glutam	Aaa12925 Human alp
ΩI	AAA65395	AAA65394	AAA65393	ACA21027	ADA29053	AAS22742	AAS22506	ACH25483	ACH28170	ABN92747	ABL26531	ADA00895	ABL26530	ABL21028	ABN35170	ADC90379	AAH65860	AAH34551	ABX43841	ABK74808	AAH65859	ACA00221	AAA12925
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Acd67251 Smooth mu Adc34675 Human smo Adc393040 E. facciu Ab161133 Human alp Ab218432 Group III Aca13595 Prokaryot Adc93095 E. facciu AAh76872 Mouse mas AAh76872 Mouse G p Axx26368 Genetic C Aas41275 CDNA enco Abra12105 CDNA enco Abra12105 CDNA enco Ab1212301 Drosophil Ab123301 Drosophil Ab214957 Arabidops Aax43879 C. vicina Aax60742 Human pol Adb48938 Novel hum Ab58956 Human pol Adb48938 Novel hum	SLNS	gene DNA sequence SEQ ID NO:7. ransporter; breeding; ATPase;		8u 7;	evibacterium lactofermentum, its encoded breeding Corynebacteria particularly for
ACD67251 ADC34675 ADC34040 ABL61139 ABL61139 ABC1139 ACA31365 AACA31643 AACA31643 AACA31647 AACA3167	ALIGNMENT	gltBD ; ABC t	alifiers ORF1" ORF2" ORF2"	9. 1. K, Nakamat AAB12593.	of Br
8 8 8 9 7 700 0 9 8 8 8 9 7 700 0 9 8 8 9 8 9 7 7 7 7 7 7 7 7 7 7 7 7 7 7	DNA; 237	evised) iirst entry) lactofermentum g lactofermentum, n; gltBD, L-glute	Location/Qual 11104 /*tag= a /*tag= n/Droduct= "OR 1117 .1728 /*tag= b //Droduct= "OR 1759 .2370 /*tag= c //product= "OR /*tag= c //product= c //pro	WO-JP00707 JP-0036062 CO INC. E, Matsuì 39;	constituent outs, applicable
	77 1 395 AAA65395 standard; AAA65395	SEP-2003 (; SEP-2003 (; NOV-2000 (; vibacterium ynebacterium ynebacterium	Key CDS CDS CDS	WO200037647-A1. 29-JUN-2060. 16-DEC-1999; 99 18-DEC-1998; 98 (AJIN) AJINOWOTO XANDO S, KIMUKA WPI; 2000-452189/ P-PSDB; AAB12591,	ABC transporter ogene and variants production of L-g
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WPI; 2000-452189/39
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                                                                                                                                                                                                                                                                                                                                                                                                                            1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITGAGICGIICGAGGAAAAGCCAGIITITIGAACICICIGGIGGGGAACAACAACGAACI 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGACAA 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1657 GGCGCCACCGTTGTTGTTGCTACGCACTCGCCCCTCTTCCGAGAATCAGCGGATACCATT 1716
                    The present invention describes a protein (I) which can be used to construct an ATP binding classette (ABC) transporter. ABC transporter DNAs can be used in breeding Corynebacteria particularly for production of L-glutamic acid. The present sequence encodes three ORFS (open reading frames) from the Brevibacterium lactofermentum gltBD gene, which is used in the exemplification of the present invention. (Updated on 15-SSP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                           CITGAGICGITCGAGGAAAAGCCAGIIITITGAACICTCTGGIGGCGAACAACAACGAACT 420
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                                                                                                                                                                                                                                                                                                                                      GAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAAATACG
                                                                                                                                                                                                                                                                                                                                                                                GTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAATTCAACCTT
                                                                                                                                                                                                                                                                                                                                                                                                      CAGCTTGCGGTGGAAAACACAAATGGCCTGAAATTCCTCAAGTACTTCATGCTGTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGACAA
                                                                                                                                                          Gaps
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                                                                                                                                                        .0
                                                                                                                                   Length 2370;
                                                                                                             Sequence 2370 BP; 633 A; 563 C; 515 G; 659 T; 0 U; 0 Other;
                                                                                                                                Match 100.0%; Score 609; DB 3; Length 2 Local Similarity 100.0%; Pred. No. 8.7e-310; es 609; Conservative 0; Mismatches 0; Indels
Claim 14; Page 23-28; 34pp; Japanese.
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The present invention describes a protein (1) which can be used to construct an AFP binding cassette (ABC) transporter. ABC transporter. DNAs can be used in breeding Corynbacteria particularly for production of Lightramic acid. The present sequence represents a PCR primer for the Brevibacterium lactofermentum gitBD gene, which is used in the exemplification of the present invention. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABC transporter constituent of Brevibacterium lactofermentum, its encongene and variants, applicable in breeding Corynebacteria particularly production of L-glutamic acid.
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corynebacterium; gltBD; L-glutamic acid; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakamatsu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 GCTCAACTGTCTTGGCACACTTGACAAACC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilarity 100.0%; Pred. No. 3.5
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA65393 standard; DNA; 22 BP
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                                                                  Corynebacterium glutamicum.
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f Brevibacterium lactofermentum, its encoded in breeding Corynebacteria particularly for
                                                                    The present invention describes a protein (I) which can be used to construct an APP binding cassette (ABC) transporter. ABC transporter can be used in breeding Corynebacteria particularly for production of glutamic acid. The present sequence represents a PCR primer for the Brevhacterium lactofermentum gltBD gene, which is used in the exemplification of the present invention. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                        ch 3.6%; Score 22; DB 3; Length 22; 1 Similarity 100.0%; Pred. No. 0.56; 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                 Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
                                              Disclosure; Page 21; 34pp; Japanese.
                                                                                                                                                                                                                                      165 CGGACAGATCCTTGTCGAGGAT 186
                                                                                                                                                                                                                                                       CGGACAGATCCTTGTCGAGGAT 1
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   ABC transporter constituent of
gene and variants, applicable i
production of L-glutamic acid.
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2001US-00948993.
2001US-0342923P.
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08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                     ACA21027 standard; DNA; 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acinetobacter baumannii.
                                                                                                                                                                                                                                                                                                                                                                                                                               drug design; gene
 ABC transporter
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                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                     Local
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Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Malone Zamudio C, Trawick JD, WPI; 2003-029926/02 P-PSDB; ABU17157 Wang L, Wall D,

(ELIT-) ELITRA PHARM INC.

Claim 14; SEQ ID NO 8897; 1766pp; English.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the

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the polypeptide of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of agene in an operon required for proliferation, (7) identifying a compound that influences the activity of proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway of a proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an orangement's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (10) profiling a product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense mucleic acids required for its proliferation or soreening for homologous mucleic acids required form discovery processed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 20;
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100.0%; Pre
0; '
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Best Local Similarity 100.
Matches 19; Conservative
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Gaps

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ADA29053 standard; DNA; 855 ADA2905.

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DNA encoding Acinetobacter baumannii protein #340. (first entry) 20-NOV-2003

ds; gene; Acinetobacter baumannii; bacterial disease; antibacterial; vaccine; plant biocontrol agent.

Acinetobacter baumannii. US6562958-B1

04-JUN-1999; 13-MAY-2003,

THERAPEUTICS CORP. 98US-0088701P. 99US-00328352 (GENO-) GENOME 09-JUN-1998;

WPI; 2003-576092/54. P-PSDB; ADA33179. Bush D; Breton G,

New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for

SEQ ID NO 340; 328pp; English Example;

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The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                              protein.
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Sequence 855 BP; 239 A; 168 C; 193 G; 255 T; 0 U; 0 Other;

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0; Gaps
Score 19; DB 8; Length 855; Pred. No. 20;
                         0; Indels
         100.0%; Pred. No. 20, rive 0; Mismatches
                                                  115 GGAAATCGACTTTGCTCA 133
                                                                             199 GGAAAATCGACTTTGCTCA 217
            Local Similarity 100.
 Query Match
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RESULT 6

Human cDNA encoding a novel human protein #308.

Human; novel protein; ss; Antianaemic; osteopathic; antiinflammatory; findunomodullatory; oytostatic; neuroprotective; vulnerary; noctropic; anticonvulsant; antiathritic; cerebroprotective; antifungal; antivities; antiallergic; dermatological; haemostatic; antiasthmatic; frombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.

Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage.

Claim 1; Page 706; 894pp; English.

The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise ASS2742/C

ASS2742/C

AAS22742/C

AAS22742;

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AAS22742;

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AAS22742;

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AAS22742;

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AUGURAN CONDITIONAL CONDITIONAL

The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for

Claim 1; Page 273-274; 894pp; English.

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antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound-healing, treating burns; promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, alzehimer's, parkinson's and Huntington's diseases, amylorrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-wersuls-sort disease, each haemophilia, thrombosis, anti-infiammatory diseases, nervous system disorders, and infection. The present sequence encodes a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, novel protein, ss. Antianaemic, osteopathic, antiinflammatory, immunomodulatory, cytostatic, neuroprotective; vulnerary, notropic; anticonvulsant, antiarthritic, cerebroprotective, antifungal, antiarthritic, terebroprotective, antifungal, antivital, antibody, gene therapy, neurological antiarthritic, thrombolytic, immunogen, antibody, gene therapy; neurological disorder; parkinson's disease; unflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
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                                                                                                                                                                                                                                                            Sequence 446 BP; 131 A; 90 C; 91 G; 134 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA encoding a novel human protein #72.
                                                                                                                                                                                                                                                                                                        100.0%; Pred. No.
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es 18; Conserv
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reading frame of the novel polynucleotide. The nucleic acid sequences

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recombinant proteins, and in generating anti-sense DNA or RNA and in generating proteins, and in generating anti-sense DNA or RNA and in generating therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands.

Colypeptides of the invention may also be useful in treating platelet disorders stem cell disorders, regenerating bone, cartilage, tendon, ilgament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, alreing stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host diseases, nervous system disorders, and infection. The present sequence encodes a protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH3631, whose sequence was determined by the technique of SBH (sequencing by hybridiation). Also included is a purified polypeptide comprising a sequence corresponding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                     Sequence 471 BP; 135 A; 96 C; 98 G; 142 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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ACH25483 standard; cDNA; 496 BP.
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Local Similarity 100.0%;
es 18; Conservation
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(LABA/) 1
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            are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The purified polypeptide is useful for generating antibodies specific for it. The present sequence for this patent did not form part of the printed specification, but was segdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH5081, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tage (EST) for identifying expressed egnes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polymucleotide sequences obtained from various cDNA libraries, user as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                          DB 8; Length 496;
69;
                                                                                                                                                                                                                                         Seguence 496 BP; 138 A; 92 C; 84 G; 165 T; 0 U; 17 Other;
                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                     100.0%; Pred. ...
                                                                                                                                                                                                                                                                            Score 18;
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DICK/) DICKSON M C. (JONE/) JONES L W.
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(STAC/)
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ACH28170/c
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responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence for the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence. html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosts and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
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                                                                                                                                                                                                    Sequence 498 BP; 141 A; 96 C; 105 G; 143 T; 0 U; 13 Other;
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                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                        Query Match 3.0%; Score 18; DB 8;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 18; Conservative 0; Mismatches (
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                                                                                                                                                                                                                                                                                                                                                             AACACAAATGGCCTGAAA 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN92747 standard; DNA; 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Doucette-Stamm LA, Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6380370-B1
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ABN92747
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABR72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                            Drosophila melanogaster genomic polynucleotide SEQ ID NO 31066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse osteoclast related protein Gl encoding cDNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 4; Length 1125;
Pred. No. 68;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 31066; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1125 BP; 304 A; 251 C; 291 G; 279 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                           Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA00895/C
ID ADA00895 standard; CDNA; 2997 BP.
IX AC ADA00895;
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DT 06-NOV-2003 (first entry)
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ABL26531 standard; DNA; 1125 BP
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                                                                                                                                                                                                                                                                                                                                                                                           Li PWD,
                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US009231.
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                              pharmaceutical; gene; ds
                                                                                                                                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                           Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY.
                                                                                                                                                                                                             WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interactions
                                                              26-MAR-2002
                                                                                                                                                                                                                                              27-SEP-2001.
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Gaps

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18; Conservative

Matches

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The present invention describes an isolated or purified nucleic acid molecule (I) encoding a mammalian Gl polypeptide which modulates bone rescorption in osteoclast cells. (I) has osteopathic activity and can be used in gene therapy. Gl genes and polypeptides are useful for preventing or treating bone related diseases such as osteopetrosis or osteoporosis, and for proper osteoclast maturation and bone tissue resorption. Probes and antibodies raised against the Gl gene product can be used in phybridisation and immunological assays to screen for and detect the presence of either a normal or mutated gene or gene product. The present sequence encodes the mouse Gl osteoclast related protein, from the
              Gl; bone resorption; osteoclast; osteopathic; gene therapy;
bone related disease; osteopetrosis; osteoporosis; osteoclast maturation;
osteoclast related protein; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                              New Gl polypeptides and genes encoding them, useful for preventing or treating bone related diseases e.g. osteopetrosis or osteoporosis, and for modulating proper osteoclast maturation and bone tissue resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genomic polynucleotide SEQ ID NO 31063.
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100.0%; Pred. No. 68;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2997 BP; 818 A; 642 C; 696 G; 841 T; 0 U; 0 Other;
                                                                                                                                              /*tag= a
/product= "osteoclast related protein GI"
                                                                                                                                                                                                                                                                                                                                                                  Benachenou N;
                                                                                                          Location/Qualifiers
45. .1061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL26530 standard; DNA; 3125 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Fig 8; 76pp; English.
                                                                                                                                                                                                                                                              25-SEP-2002; 2002WO-EP010721.
                                                                                                                                                                                                                                                                                                27-SEP-2001; 2001CA-02357987.
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Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                              (AVET ) AVENTIS PHARMA
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-381602/36.
P-PSDB; ADA00896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention.
                                                                                                                                                                                                WO2003029283-A2
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                                                                                Mus musculus,
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                                                                                                                                                                                                                              10-APR-2003
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of disciolase, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB7737-ABB72072). The sequence data for this pattent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 4; Length 3125;
Pred. No. 68;
                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 31063; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3125 BP; 966 A; 597 C; 649 G; 913 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL21028 standard; DNA; 11920 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          583 GAATCAGCGGATACCATT 600
                                                                                                                                       PWD,
                              23-MAR-2001; 2001WO-US009231.
                                                          2000US-0191637P.
2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                   Venter JC, Adams M,
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                                                                                                                                                                 WPI; 2001-656860/75.
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                                                          23-MAR-2000;
11-JUL-2000;
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20-JUL-2001; 2001WO-IB001903.
                                 Homo sapiens.
                                       07-FEB-2002
                                                       Shoshan A,
                  ABN35170;
Matches
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention siscloses genomic DNA sequences (ABL16511), expressed DNA sequences (ABL16175-ABL36511), expressed DNA sequences (ABL10810). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11920 BP; 3521 A; 2455 C; 2509 G; 3435 T; 0 U; 0 Other;
                                               Claim 1; SEQ ID NO 14557; 21pp + Sequence Listing; English.
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Gaps 0 3.0%; Score 18; DB 4; Length 11920; 100.0%; Pred. No. 67; 0; Indels () 373 GAGGAAAGCCAGITITI 390 Best Local Similarity 100. Matches 18; Conservative Query Match

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2140 GAGGAAAAGCCAGTTTT 2123

ABN35170 standard; DNA; 60 BP.

(first entry) 15-JUL-2002

Human spliced transcript detection oligonucleotide SEQ ID NO:7918. Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.

WO200210449-A2.

28-JUL-2000; 2000US-0221607P. 02-MAY-2001; 2001US-0287724P.

(COMP-) COMPUGEN INC

New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-Faigler S; Mintz L, Mintz E, Wasserman A, WPI; 2002-257383/30.

Example 1; SEQ ID NO 7918; 47pp; English

specific genes.

The present invention describes oligomuclectide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligomuclectides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligomuclectide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in

detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcriptome under a particular biological or pathological state, and so allowing the detection of tissue and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular tate, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pot_sequences ò Gaps .. 0 Length 60; Score 17; DB 6; Length 60; Pred. No. 2.4e+02; 0; Mismatches 0; Indels Sequence 60 BP; 16 A; 15 C; 15 G; 14 T; 0 U; 0 Other; Query Match
2.8%; Sor
Best Local Similarity 100.0%; P.
Matches 17; Conservative 0; 373 GAGGAAAAGCCAGTTTT 389 59 GAĞĞAAAĞCCAĞTTT 43 \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$ ò

Search completed: July 30, 2004, 15:35:53 Job time: 457 secs

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RESULT 2
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                                                                                                                                                 July 30, 2004, 15:19:50 ; Search time 99 Seconds (without alignments) 3413.789 Million cell updates/sec
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6: /cgn2_6/ptodata/2/ina/PacKfIles1.seg:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-107-532A-3137

US-09-1312-94-58

US-09-131-294-1004

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                                                                                                   nucleic search, using sw model
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Match Length
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Perfect score:
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Maximum DB
                                                                                                 OM nucleic
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                                                                                                                                                                                                                                                                                                        Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
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Sequence 2210, Application US/09134001C

| Parent No. 6380370
| Parent No. 6380370
| Parent No. 6380370
| APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al ITILE OF INVENTION: WICHER ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
| TITLE OF INVENTION: WICHER, 2007 134,001C
| TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: USBER: US 60/064,964
| FILE REPERENCE: GTC-07
| CURRENT FILING DATE: 1997-11-08
| PRIOR FILING DATE: 1997-11-08
| PRIOR FILING DATE: 1997-08-14
| NUMBER OF SEQ ID NOS: S674
| NUMBER OF SEQ ID NOS: S674
| TYPE: DNA | TYPE: DNA |
| TYPE: DNA | TYPE: DNA |
| CORGAMISM: Staphylococcus epidermidis | US-09-134-001C-2210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
US-09-328-352-340
US-09-328-352-340
US-09-328-352-340
US-09-328-352-340
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US-09-328-352
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             11258, Ap
48, Appl
200, Ap
6060, Ap
6060, Ap
111, Appl
111, Appl
113, Appl
113, Appl
114, Appl
117, Appl
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US-09-833-381-1258
US-09-833-381-48
US-09-833-381-48
US-09-833-381-1255
US-09-543-6016-29
US-09-134-6016-29
US-09-833-381-1259
US-09-833-381-1250
US-09-833-381-1250
US-09-833-381-1250
US-09-211-1260
US-09-374-038-13
US-09-374-038-11
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3.1%; Score 19; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 19; Conservative 0; Mismatches
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ORGANISM: Acinetobacter baumannii
US-09-328-352-340
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Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAF
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
                         APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: Chandler, Lois Ann
APPLICANT: Chandler, Lois Ann
APPLICANT: Chandler, Lois Ann
APPLICANT: Compositions Compositions Containing NUCLEIC ACIDS AND LIGANDS FOR THERAPE
NUMBER OF SEQUENCES: 128
CORRESSEONDERSS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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COUNTRY: USA
ZIP: 98144-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 24-No. 6503866-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                               Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.8%; Score 17; DB 3;
100.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: No. 6037329tenburg Ph.D., Carol
REGISTRATION NUMBER: 39.317
REFERENCE/DOCKET NUMBER: 39.317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION UNMERS: US/08/718,904
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-Gyray-243-109, Application US/09449249
Patent No. 6503886
GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
Chandler, Lois Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.00,
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206) 622-490
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 700 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
                                                                                                                                                                                                  Washington
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Matches 17; Conserv
             GENERAL INFORMATION:
                                                                                                                                                                                Seattle
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                                                                                                                                                                            CITY: Sec
STATE: WE
COUNTRY:
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                                                                                                                                                                              Sequence 6, Application US/09107532A
Sequence 6, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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100.0%; Pred. No. 26;
tive 0; Mismatches 0; Indels
                   Indels
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS: ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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   Pred. No. 7.9;
                   Mismatches
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LOCATION: (B) LOCATION 1...192
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-08-718-904-109
; Sequence 109, Application US/08718904
                                                                                                                                                                                                                                                                                                                                                          STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                 , 0
                                                         247 TATTTATTTCAAGATTAT 264
                                                                                           238 TATTTATTTCAAGATTAT 255
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                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
   Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                            CITY: Waltham
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Best Local Similarity
Matches 17; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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US-09-107-532A-6/c
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Gaps

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Sequence 2722, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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2.8%; Score 17; DB 4; Length 711;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 7110
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.,
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR, APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: 14 May 1998
ATTORNEY/AGENT INFORMATION:
NAME: Arimiello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
TELECOMMUNICATION INFORMATION:
TELEPRAM: (781) 893-507
TELECOMMUNICATION INFORMATION:
TELEPRAM: (781) 893-507
TELEPRAM: (781) 893-507
TELECOMMUNICATION INFORMATION:
TELEPRAM: (781) 893-8277
INFORMATION FOR SEQ ID NO: 2722:
SEQUENCE CHARACTERISTICS:
LENGTH: 858 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.8%; Score 17; DB 4;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0
                                            NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...711
; SEQUENCE DESCRIPTION: SEQ ID NO: 2667:
US-09-107-532A-2667
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LOCATION: (B) LOCATION 1...858
SEQUENCE DESCRIPTION: SEQ ID NO: 2722:
     ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPÓLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 858 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                           466 GATGAACCAACCGGAGC 482
                                                                                                                                                                                                                                                                                                                                             277 GATGAACCAACCGGAGC 293
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-107-532A-2722
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Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                  APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-196
ATTORNEY/AGENT INPOMATION:
NAME: No. 650386fenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.8%; Score 17; DB 4;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8077
INFORMATION FOR SEQ ID NO: 2667:
                                                                                                                                                                                                                                                                                                                                                          TOPOLGY: 1100 SEQUENCE DESCRIPTION: SEQ ID NO: 109: US-09-449-249-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 AAATGGCCTGAAATTCC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 AAATGGCCTGAAATTCC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
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  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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US-09-107-532A-2667
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Gaps
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TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REPREDENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/09/620,312D
                                                                                                       CURRENT APPLICATION OF ACCURAGE OF ACCURAGE ACCIT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/05151
ATTORNEY/AGAIT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 47-012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
;
; SEQUENCE DESCRIPTION: (B) LOCATION 1...1497
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US-09-107-532A-3337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-620-312D-848/c
, Sequence 848, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAK: (781)893-8277
INFORMATION FOR SEQ ID NO: 3337:
SEQUENCE CHARACTERISTICS:
LENGTH: 1497 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AAATCGACTTTGCTCAA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yang, Yonghong
Wang, Jian Rui
Zhou, Ping
Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kue, Aidong J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
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Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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2.8%; Score 17; DB 2; Length 1127;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                  RESULT 8
US-07-35-068-1
| Sequence 1, Application US/07735068
| Patent No. 5885769
| Patent No. 58857696|
| GENERAL INFORMATION: No. 58857696| Screening Systems TITLE OF INVENTION: No. 58857696| Screening Systems OWNERS OF SQUENCES: 4 NUMBER OF SQUENCES: 4 NUMBER OF SQUENCES: 4 STREE: One Giralda Farms | STREE: New Jersey COUNTRY: USA | COUNTRY | COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: New COLOGY

COUNTRY: USA

ZIP: 07940-1000

COMPUTER READABLE DEPOY disk

COMPUTER: READABLE Macintosh

OPERATING SYSTEM: Macintosh

OPERATING SYSTEM: Macintosh

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/735,068

FILING DATE: 19910724

CLASSIFICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION NUMBER: US07/655966

FILING DATE: 14-FEB-1991

ATTORNEY AGENT INFORMATION:

NAME: DULAK, NO. 5885769man C.

REGISTRATION NUMBER: 1100178K

TELECAMONICATION NUMBER: 1D0178K

TELECAMONICATION INFORMATION:

TELECAMONICATION NUMBER: 1D0178K

TELECAMONICATION NUMBER: 1D0178K

TELECAMONICATION NUMBER: 1D0178K

TELECAMONICATION NUMBER: 1D0178K

TELECAMONICATION NUMBER: 1100178K

TELECAMONICATION NUMBER: 1D0178K

TELECAMONICATION NUMBER: 1
                                           109 GGTTCAGGAAAATCGAC 125
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                                                                                                                         145 GGTTCAGGAAAATCGAC 161
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STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-07-735-068-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-107-532A-3337
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STRANDEDNESS: double
                                                                                                                                                                                                                                                  US-09-347-878-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-08-961-527-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-961-527-94
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Sequence 5, Application US/09468656A

GENERAL INPORMATION:

APPLICANT: Johnson, Leslie S.

APPLICANT: Adamou, John E.

TITLE OF INVENTION: Wactine Compositions Comprising Streptococcus

TITLE OF INVENTION: Motife

TITLE OF INVENTION: WIMBER: 05/01-444

CURRENT APPLICATION NUMBER: 06/113,048

PRIOR APPLICATION NUMBER: 60/113,048

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.1
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Patent No. 6376210

GENERAL INFORMATION:

TILLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES

FILLE REPREBNCE: 25885-1651

CURRENT FILLING DATE: 1999-07-06

NUMBER OF SEQ ID NOS: 75

SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 28;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   2.8%; Score 17; DB 100.0%; Pred. No. 28; tive 0; Mismatches
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 848
LENGTH: 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-468-656A-5
                                                                                                                                                                                                                                                                                                                 CCATION: (1).T.(2351)
CTHER INFORMATION: n = a,t,c or g
US-09-620-312D-848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1981 ÁGGAAAAGCCAGTTTT 1965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 AGGAAAAGCCAGTTTTT 390
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 17, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (46)..(1422)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-468-656A-5
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LENGTH: 2531
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US-09-347-878-25
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GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
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| SEQ ID NO 25
| LENGTH: 2561
| TYPE: DNA
| ORGANIGN: Escherichia coli
| FRATURE:
| NAME/KEY: CDS
| LOCATION: (1131)..(2399)
| OTHER INFORMATION: Follypolyglutamate synthetase-dihydrofolate
| OTHER INFORMATION: synthetase
| PUBLICATION INFORMATION:
| PUBLICATION INFORMATION:
| DALICATION OF COLORS | M32445/GenBank
                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                         DB 4; Length 2561; 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17; DB 4; Length 8195;
Pred. No. 29;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER FABBABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectre 486/33
OPERATING SYSTEM: MSDGS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                    Query Match

2.8%; Score 17; DB
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: GALO KESS:
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 94, Application US/08961527
Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brockes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1116 GAATCAGCGGATACCAT 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.8%; Soc
Best Local Similarity 100.0%; Pr
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                         583 GAATCAGCGGATACCAT 599
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.6%; Score 16; DB 4; Length 183; Best Local Similarity 100.0%; Pred. No. 91; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.6%; Score 16; DB 3; Length 255; Best Local Similarity 100.0%; Pred. No. 91; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNALL THE PARTICAL TO NO SERVING BELLOHAND SEQUENCE 58, Application US/08821994A

PRICAL NO 6228643

GENERAL INFORMATION:
APPLICANT: Thomas, Didler RP
APPLICANT: DEPOND 1897

CURRENT APPLICATION NUMBER: US/08/821,994A

CURRENT RILING DATE: 1997-03-18

EARLIER APPLICATION NUMBER: GB 960662.9

EARLIER PILING DATE: 1996-03-22

NUMBER OF SEQ ID NOS: 89

SOFTWARE: PARENTIN VOY: 2.1

SEQ ID NO 58

LENGTH: 255

LENGTH: 255

CORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                    ORGANISM: Staphylococcus epidermidis US-09-134-001C-1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
CCATION: 136, 187, 192
CTHER INFORMATION: n is unknown
US-08-821-994-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                            480 AGCTCTAGATTTAACA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 AGCTCTAGATTTAACA 138
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US-08-821-994-58/c
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RESULT 14
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Search completed: July 30, 2004, 17:25:10 Job time : 100 secs

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July 30, 2004, 15:13:30 ; Search time 2790 Seconds (without alignments) 6518.304 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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609
                                                                            OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
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BST:*

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2: em_estba:*
3: em_estin:*
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5: em_estcu:*
6: em_estcu:*
7: em_estcu:*
10: gb_est1:*
11: gb_est1:*
11: gb_est2:*
11: gb_est2:*
11: gb_est2:*
12: gb_est2:*
13: em_estfun:*
14: gb_est5:*
14: gb_est5:*
15: em_estfun:*
16: em_gss_fun:*
17: em_gss_fun:*
18: em_gss_fun:*
18: em_gss_fun:*
19: em_gss_fun:*
18: em_gss_fun:*
19: em_gss_fun:*
22: em_gss_fun:*
24: em_gss_fun:*
25: em_gss_fun:*
26: em_gss_fun:*
27: em_gss_fun:*
28: gss_fun:*
29: em_gss_fun:*
20: em_gss_fun:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		AV279945 AV279945	AV283498 AV283498	BB522412 BB522412	AW319130 un03f03.x
SUMMARIES			1D		AV279945	AV283498	BB522412	AW319130
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0 AW2105	AI57387	A187467	AW01256	AI31734	AA39704	AA26049	3 BX6351	0 BB69060	AI42759	0 BB7478	AA25058	0 BB7485	3 BQ62160	AA27495	AA11289	AI18200	AI19681	AI04294	AI03565	2 BG7028	AI32638	AI04669	AI25582) BB6029	0 BB21709	AL82319	D BF65927	9 BX12485	3 BQ76717	3 BQ44403	1 CD56433	3 AQ87391	3 BH35032	1 CA53379	3 BZ69410	3 CG80723	2 BI98846	3 BU702558	CP25750	CD56207
62 1	68	79	83	32	17	27	40 1	45 1	55	63 1	64	71 1	78 1	81	04	18	69	8	11	8	4.	74	54	49 1	1 90	11 9	19 1	22 2	28 1	14 1	44 1	52 2	57 2	30 1	35 2	96 2	00	600 13	34 1	1 62
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ALIGNMENTS

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Fukuda, S., Fukunishi, Y., Hara, B., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hari, F., Kaduda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hari, F., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Kodora, K., Kagawa, I., Marsiyama, T., Mixuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Okaya, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Sugahara, K., Suzuki, H., Suzuki, H., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tounoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yoshikide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushino-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was cloned into the XhoI and BanHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BanHI."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             propared and sequenced in Mouse Genome Encyclopedia propared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues, 1st strand cDNA was GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTVN 3'), cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh.M., Kitsunai, T., Athyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Akazaki, Y., and Hayashizaki, Y.
Akazaki, Y. and Hayashizaki, Y. Akazaki, Y. Akazaki, Y. Akazaki, Y. and Hayashizaki, Y. Akazaki, Y. Akazaki,
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(DR108)"
                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 244)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primer adapter of sequence [5' GAGAGAGAGATTCTCGCCCCCCC 3']. cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carning, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9; Length 244;
32;
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            further details.
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Best Local Similarity
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            ORGANISM
                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Comaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayanizaki, Y., Ozawa, Y., Muramatsu, M., Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Garninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(58C), Yokohama Institute April 100 to 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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fmol type="mxRNA"
strain="CS7BL/6"
/db_xref="taxon:10090"
/clone="4933411H02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="testis"
/dev_stage="adult"
/lab_host="DH108"
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                                                                                                                                                                                                                       Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV283498/c
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KEYWORDS
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/note="Site 1: Sall; Site 2: BamHI: cDNA library was prepared and sequenced in Nouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5] grader of sequence [5] grader of sequence [5] grader of sequence [5] grader [5] grader of sequence [5] grader [5] gra
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
/lab_host="DHIUB"
/clone_lib="Sugano mouse kidney mkia"
/hote="Organ: kidney; Vector: pME188-FL3; Site 1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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High quality sequence stop: 345.
Location/Qualifiers
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/strain="C57BL"
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AUTHORS
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (360), Yokohama Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan
1-7-22 Suchiro-cho, Japan
1-7-7-22 Suchiro-cho, Japan
1-7-7-2
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Mus musculus (bouse mouse)

Mus musculus Eutheria, Redardia, Craniata, Vertebrata; Euteleostomi,

Budaryota; Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,

Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.

E. (bases 1 to 303)

Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T.,

Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,

Izawa, M., Kadota, K., Kagawa, J., Kahi, C., Kawai, J., Ishikawa, T., Itoh, M.,

Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,

Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamira, M., Oda, H.,

Okazaki, Y., Ono, T., Owa, C., Saitoh, H., Sakai, C., Satoh, K.,

Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,

Takahashi, F., Tominaga, N., Suzuki, H., Suzuki, H., Tagawa, A.,

Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,

Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB522412 RIKEN full-length enriched, 15 days embryo head Mus musculus CDNA clone D930007074 3' similar to AJ011080 Mus musculus character in RNA sequence.
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                                        0; Gaps
                                        0; Indels
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/dev_stage="15 days embryo"
/lab_host="DH10B"
                                  0; Mismatches
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Unpublished (2000)
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/mol type="mRNA"
/strain="C578L/63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xref="taxon:10090"
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                                                                                                                                           382 CCAGTITITGAACTCTCTGG 401
                                                                                                                                                                                                                                        59 ccadririrgaacrereigg 40
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BB522412.1 GI:9573870
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                                  20; Conservative
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BB522412/c
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3.3%; Score 20; DB 9; Length 368;
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                                                                                                                                                               Query Match
Best Local &
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was primed with an oligo(dT) primer [ArGTGGCCTTTTTTTTTTTT]; double-stranded cDNA was ligated to a Drall adaptor [TGTTGGCCTACTGG], digested and cloned into distinct Drall sites of the pME185-F13 vector (5' site CACTGTGG, 3' site CACCATGTG). Xhol should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCACA."
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/note="logan: kidney; Vector: pME185-FL3; Site_1: DraIII
(CACGATGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
(KACTGCTGCTTTTTTTTTTTTTTTTTT); double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGCTACTACTGG), digested
and cloned into distinct DraIII sites of the pME185-FL3
be used to isolate the CDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AWALUDBI 362 bp mRNA linear EST 03-DEC-195 um62all.xl Sugano mouse kidney mkia Mus musculus cDNA clone INAGE:2285948 3' similar to SW:AFAM_MOUSE 089020 AFAMIN PRECURSOR AND ASSETT OF A MANA SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryora, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalla, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 322)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Onderwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,T., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The WashU-Nor Mouse EST Project 1999
Unpublished (1999)
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Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                  3.3%; Score 20; DB 10; Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
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/sex="female"
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Location/Qualifiers
1, .362
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/lab_host="DH10B"
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/strain="C57BL"
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Fax: 314 286 1810
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AW210581
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VERSION

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constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAGGTGGG and 3' end primer CGACCTGCAGGCACA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AI573872 368 bp mRNA linear EST 29-MAR-1999
uj17d06.x1 Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:1908299 3' similar to SW:AFAM_RAT P36953 AFAMIN PRECURSOR ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryotan Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria; Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 368)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Onderwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R., The WashUncI Mouse BST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.linl.gov) for further information. MGI:976495
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fer: 314 256 1800
Fax: 314 286 180
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                            0
                                                                                                                                                       3.3%; Score 20; DB 10; Length 362; 00.0%; Pred. No. 33;
                                                                                                                                                                                                            0; Indels
                                                                                                                                                          Similarity 100.0%; Pred. No. ...
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/mol type="mRNA"
/strain="C57BL"
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/clone="IMAGE:1908299"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                       168 ccadririrdaacrered 187
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Mus musculus
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Matches

ò g DEFINITION

A1874676 RESULT 7

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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/clone_libe_sugano mouse kidney mkia"
/clone_libe_sugano mouse kidney mkia"
/note="Grgan: kidney; Vector: pME185-F13; Site_1: DrallI
(CACTGTGTG); Site_2: Drall! (CACCATGTG); 1st & Trand cDNA
was primed with an oligo(dT) primer
was primed with an oligo(dT) primer
| ATGTGGCCTTATTTTTTTTTTTTTTT]; double-stranded cDNA was
| igated to a Drall! adaptor [IGTTGGCTACTGG]; digested
and cloned into distinct Drall! sites of the pME185-F13
vector (5' site CACTGTGT, 3' site CACTATGTG); Xiol & Site CACTATGTG, Site Selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTICTGCTCTAAAAGCTGCG and 3' end
                                                                                                                                                   183 bp mRNA linear EST 10-SEP-1999 ul69al0.x1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2135802 3' similar to TR:089020 089020 ALPHA-ALBUMINE PROTEIN, ; mRNA sequence.
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other ESTS: ul69a10.y1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
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100.0%; Pred. No. 33;
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/mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="taxon:10090"
/clone="IMAGE:2135802"
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Location/Qualifiers
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/lab_host="DH10B"
                                       CCAGTTTTGAACTCTCTGG 205
                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Matches 20; Conserv
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//dev stage="adult"
//deb_host="DH10B"
//clone_lib="Sugano mouse kidney mkia"
//clone_lib="Sugano mouse kidney mkia"
//note="Organ: kidney; Vector: pME186-FL3; Site_1: DraIII
//note="Organ: kidney; Vector: pmE186-FL3; Site_1: DraIII
//note="Organ: kidney; Vector: pmE186-FL3; Site_1: DraIII
//note="Organ: kidney; Vector: pmE186-FL3; Site_2: DraIII (CACCATGTG); ist stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG]; digested
and cloned into distinct DraIII sites of the pME186-FL3
vector (5' site cACTGTGG); 3' site CACCATGTG; Xhol should
be used to isolate the cDNA innert. Size selection was
performed to exclude fragments <-1.5bc Library
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Moferwood,K., Steptoe,M., Theising,B., Allan,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL , contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                   Gaps
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                                                                                                                                                                                                                                                                                                               AI874676
379 bp mRNA linear EST 21-:
ul25a10.Xl Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:2099322 3' similar to TR:089020 089020 ALPHA-ALBUMINB
PROTEIN, ;, mRNA sequence.
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                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M.WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
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                                 Pred. No. 33; Mismatches
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High quality sequence stop: 368.
Location/Qualifiers
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/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2099322"
                                                                                                                                                      174 CCAGTTTTTGAACTCTCTGG 193
                                                                                                              382 CCAGTTTTGAACTCTCGG 401
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100.0%; Pre-
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                                                          20; Conservative
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Fax: 314 286 1810
                           Best Local Similarity
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source

FEATURES

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382
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AA260497/c
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                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 392)
Arara,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 ujlle04.xl Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:1907934 3' similar to SW:AFAM_RAT P36953 AFAMIN PRECURSOR ;,
                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:976130
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                                                                                                                                                                                                                                                                                          Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
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100.0%; Pred. No. 33;
tive 0; Mismatches 0; Indels
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/mol_type="mRNA"
/strain="C57BL"
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/clone="IMAGE:1907934"
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/lab_host="DH10B"
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EST.
Mus musculus (house mouse)
                                                                                                        Mus musculus (house mouse)
                                                                       AI317342.1 GI:4032609
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                                         mRNA sequence.
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Best Local Simil
Matches 20; C
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AA397040/c
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42/ bp mRNA linear EST 18-MAR-1997 va95g10.rl Soares mouse NML Mus musculus cDNA clone IMAGE:747234 5/ similar to SW:AFAM_RAT P36953 AFAMIN PRECURSOR ;, mRNA sequence. AA260497
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(bases 1 to 427)

Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 417)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gaclsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Chordata, Craniata, Vertebrata, Buteleostomi,
Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                     The WashU-HMMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
WashIngton University School of MedicineP
Tal: 314 286 1810
Eax: 314 286 1810
Email: mousesestGwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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100.0%; Pred. No. 33;
iive 0; Mismatches
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
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The WashU-HHMI Mouse EST Project
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Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:693089"
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/lab_host="DH10B"
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Mus musculus
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Best Local Similarity
Matches 20; Conserva
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Gaps

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Unpublished (2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contactory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Email: genome-resegger.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB690607 BIKEN full-length enriched, 12 days embryo female mullerian duct Mus musculus cDNA clone 6820448P03 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Akimura, T. Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Akakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayareu, M., Hiamoto, K., Hiraoka, T., Hirozane, T., Imocani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sakai K., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Tamaka, T., Tomaru, A., Toyawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y., Watahiki, A., Yasunishi, A., RIKEN Encyclopedia of Mouse Full-length CDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                            Length 440;
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                                                                                                                                                                                                                                                                            3.3%; Score 20; DB 1
100.0%; Pred. No. 33;
ive 0; Mismatches

    .440
    /organism="Mus musculus"

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                                                                                                                                                                                                                                                                                                                                                       Conservative
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es 20; Conserv
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BB690607/c
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AUTHORS
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KEYWORDS
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BX635140 pBluescript Lion Mus musculus cDNA clone LIOND462D02381
3', mRNA sequence.
BX635140. GI:33615015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
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Henrich, J., Hermanns, J., Kranz, H., Loebbert, R., Schlueter, T., Schuette, D., Weindel, M., Heil, O., Ebert, L., Neubert, P., Peters, M., Radloft, U., Schneider, D. and Korn, B.
Mouse ArrayTAG onna (110N)
Contact: Ina Rolfs
RZED Deutsches Ressourcenzentrum fuer Genomforschung GmbH
In Neuenhaimer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This content is available royalty-free from RZPD; content RZPD (clone@rzpd.de) for further information. Seq primer: RP: CAGGAAACAGCTATGAC.
                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:456218
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Heubnerweg 6, D-14059 Berlin, Germany
121: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
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          Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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100.0%; Pred. No. 33;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                  1. .427
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/clone="IMAGE:747234"
/tissue_type="tiver"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                  High quality sequence stop: 406.
Location/Qualifiers
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RZPDLIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 20; Conserv
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ORGANISM
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Gaps ٠,

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3.3%; Score 20; DB 9; Length 455; 100.0%; Pred. No. 33; ive 0; Mismatches 0; Indels.
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      High quality sequence stop: 358.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 CCAGTTTTTGAACTCTCTGG 401
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BB747871/c
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                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                      455 bp mRNA linear EST 07-WAR-2000 mm20h02.x1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:522099 3' similar to SW:AFAM_RAT P36953 AFAMIN PA1427549.
                                                                                                                                                                                                                                                                  /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was GAGAGAGAGACTCTTTTTTTTTTTTTVN 3''), cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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/lab_host="DH10B"
/clone_ib="mrkkw full-length enriched, 12 days embryo
female_mullerian duct"
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Moferwood,K., Sreptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL, contact the IMAGE Consortium (info@image.llnl.gov) for further information. This clone was previously sequenced on the 5' end only, this new data is from the 3' end
Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Feb 100, 1999 this sequence version replaced gi:4060832. On Feb 100, 1999 this sequence version replaced gi:4060832. Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, U Fax: 314 286 1810
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                                          'organism="Mus musculus"
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                                                                                                   db_xref="taxon:10090"
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    Location/Qualifiers
                                                           /mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                 /sex="female"
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Best Local Similarity
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JOURNAL
COMMENT
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AUTHORS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae, Murinae, Mus. 1 (bases 1 to 463)
8 Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramcho,K., Hirackan,T., Hirozana,T., Rouda,M., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Okazaki,Y., Sakai,X., Sakai,K., Nomura,K., Numasaki,R., Okazaki,Y., Satio,R., Sakai,C., Sakai,K., Sakai,X., Sakai,K., Sakai,X., Sakai,X., Sakai,X., Sakai,Y., Sakai,Y., Sakai,Y., Sakai,Y., Sakai,Y., Sakai,Y., Sakai,Y., Sakai,Y., Toyai,Y., Toyai,Y., Toyai,Y., Toyai,Y., Toyai,Y., Toyai,Y., Yasunishi,A., Muramatsu,M. and Hayashiani,Y. Watahiki,A., Yasunishi,A., RIKER Encyclopedia of Mouse Full-length cDNAS (Akimura,T., et al.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res..
BB747871 BF747871 RIKEN full-length enriched, adult male kidney Mus musculus cDNA clone F530208A04 3', mRNA sequence.
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Xonno.H., Furnishily. Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a norredundant cDNA library Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

Location/Qualifiers

Locati
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Ouery Match
3.3%; Score 20; DB 10; Length 463;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 0; Indels

Oy 382 CCAGTTTTGAACTCTTGG 401

Db 284 CCAGTTTTTGAACTCTTGG 265

ORIGIN

Gaps

. 0

> Search completed: July 30, 2004, 17:23:28 Job time : 2797 secs

Mis Page Brank (Uspic)

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July 30, 2004, 07:14:14 ; Search time 3631 Seconds (without alignments) 7269.597 Million cell updates/sec
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1 atgatagaaatcaatgacct.......cggataccattatcaaacta 609
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                   OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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2: gb_htg;*

3: gb_om:*

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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Zhu, L., Chu, L., Kogan, Y., Chaga, O., Goltsman, E., Bernal, A.,

Larsen, N., D'Souza, M., Walunas, T., Pusch, G.D., Haselkorn, R.,

Fonstein, M., Kyrpides, N. and Overbeek, R.

Direct Submission

Submitted (I.3 - FBS-2002) Integrated Genomics, 2201 W. Campbell Park

Drive, Chicago, IL 60612, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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Zhu,L., Vasieva,O., Chu,L., Kogan,Y., Chaga,O., Goltsman,E., Bernal,A., Larsen,N., D'Souza,M., Walumas,T., Pusch,G., Haselkorn,R., Fonstein,M., Kyrpides,N., and Overbeek,R. Genome sequence and analysis of the oral bacterium Fusobacterium
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        690 TTCAAGTAAGAAAAGGTGAATAGGGTTGCAATAATGGGTTCATCTGGTTCGGGAAAAATCAA 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       510 GATTAATATTTCAACAATTCCATTTAATTCCTTATTTAACTGCTCTTGAAATGTAATGG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10460. .11161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 ATGTAGACCTTCTGAAACTCTACGCGTAAGCAACGGTTATACAGGAAAAATACGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACAGGATATTACAAAAGAAAGTCAAAATTCTTTAACAAAATAAGAAGAAAAAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          750 regalgiaaaaargiereraaarararargeagarirracargeriraaaagaagriraarr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299;
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EX248355

S41553 bp DNA linear BCT 06-NOV-2003

Corynebacterium diphtheriae gravis NCTC13129, complete genome;

BX248355 BX248353

BX248355 BX248353

BX248355 L GI:38199254

S complete genome;

Corynebacterium diphtheriae

Corynebacterium diphtheriae

Corynebacterium diphtheriae;

Corynebacterium diphtheriae

Corynebacterium diphtheriae

Sallen, N., Entley, S.D., Besta, G.S., Churcher, C., Holden, M.T.G.,

Pallen, M., Bentley, S.D., Besta, G.S., Churcher, C., James, K.D., De

Zoysa, A., Chillingworth, T., Cronin, A., Dowd, L., Feltwell, T.,

Hamlin, N., Holroyd, S., Jagels, K., Thomson, N.R., Unwin, L.,

Rabbinowitsch, E., Rutherford, K., Thomson, N.R., Unwin, L.,

Whitehad, S. and Barrell B.G. Parkhill, J.

The complete genome sequence and analysis of Corynebacterium

diphtheriae NCTC13129

Nocleic General Corynebacterium

Nocleic General Corynebacterium

Associate Res. 31 (22), 6516-6523 (2003)
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1. 341553

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| forganism="Corynebacterium diphtheriae"

| forganism="McTC13129"

| db xref="taxon:171"

| force="biotype gravis"

| complement(351. 1163)

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| locus tag="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535
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                                                 476 CCGGAGCTCTAGATTTAACAACAGTGAGCTAGTCATAGAAGCATTGAGAGCAÇTCGCCG
                                                                                                                                                                                                                                            270 CAGGAAACCTIGAIGAAGIAAAIGAAAAAATIGIIAAAAAAIAITAAAAACAITCAIA
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416 GAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCGAATAATTCTGGCTGATGAACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 596 CCATTATCAAACTA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 GAAAAATATATTA 137
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KEYWORDS
SOURCE
ORGANISM
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BX248355/c
LOCUS
DEFINITION
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PUBMED
REFERENCE
AUTHORS
TITLE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDGFIRLVSRIKEIIITGGFNVYPABVĒBALIAHPDVDDAAVVGRPRKDGSEDVVACI
VLKDGAALDPEGLKTHCRKLLTRYKVPRTFYHFBALNKDQLGKVRRREVQQTILIERLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQQLALRIPIPPIAAKREQLTAFADNTVPWSTLIGNAIGGNGKRTBFPKVTKDDIALI
LYTSGTTGTPKGALLSHGNLVSNCFMGKAWVPGLGDQPBRFLAALPMFHAYGMTWVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       long-chain-fatty-acid--CoA ligase Fadb or Oldb or B1805 SW-LCFA BCOLI (P29212) (561 aa) fasta scores: E():
78e-63, 34.69% id in 565 aa. Possible duplication of the upstream CDS: Similar to DIP0386 (568 aa) fasta scores: E(): 1.2e-164, 73.488% identity in 562 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQQALLRLPIPMIRKKRDALTASAPNTIPWEILVGSALGGNGDDIVPCPEVTKKSIAL
                        long-chain-fatty-acid-CoA ligase FadD or OldD or B1805 SW:LCFA ECOLI (P29212) (561 aa) fasta scores: E(): 7.5e-62, 34.46% id in 560 aa. Possible duplication of the E()» 1.2e-164, 73.48% identity in 562 aa overlap" /codon start=1 //transI_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus tag="IIF0386"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(5953. .5988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(5164. .6486)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (4942. .6642)
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complement (4942. .6642)
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             to Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'trans]_table=11
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6726. .8009
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transl_table=
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complement(1179..1640)

/locus tag="DIP0383"

/note="Low similarity to Mycobacterium tuberculosis
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MTCX2069.07c SW:Y481 MYCTU (Q11147) (174 aa) fasta scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2806..3171)
/locus_tag="DIP0385"
complement(2806..3171)
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/locte="Similar to Bacillus subtilis YjqA protein TR:034593
(EMBL:Z99110) (125 aa) fasta scores: E(): 5e-11, 35:51% id
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in 107 aa"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEISDVLVSVTLLERATGAVMEVPAADLELAYRYSNLKFTGRGVVLGITLQIHTDGMS
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ESVGDHVRSVVGDESMPCFAAGBGMVKLSAAWLIDRAGFAKGHQGPGGRVSLSTKHTL
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UDP-N-acetylenolpyruvoylglucosamine reductase, FAD-binding
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/note="Similar to Mycobacterium tuberculosis
UDP-N-acetylenolpyruvoy/glucosamine reductase MurB or
RV0482 or MT0500 or MT072069.08 SW:MURB_MYCTU (Q11148)
(369 aa) fasta scores: E(): 1.7e-39, 51.27% id in 353 aa,
and to Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UDP-N-acetylenolpyruvoylglucosamine reductase MurB or
B3972 SW:MURB ECOLI (P08373) (342 aa) fasta scores: E():
3.1e-14, 31.69% id in 325 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(2809. _2820)
Jocus_tag="DIP0385"
/note="GranRegExp hit to PS00294, Prenyl group binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTNRGNATTDDLVALAREVRGGVMDAFGVLLEPEPVWVGVSI"
                                                                                                                                                                                                                                                                                                     product="Conserved hypothetical protein"
protein id="CAB48887.1"
db_xref="GI:38199256"
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complement (3174, .4880)
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trans1 table=
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SKITTFILKGENFSTVIMPIUM"
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ASDVFSLFMGDEVEPRRAYIQDHAKDVKHLDV"
                                                                                                                                                                                                                                                                                                                                  chromosomal
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locus_tag="WS0000"
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codon start=1
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locus tag="WS0002"
561. .4879
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                                                                                                                                                                                                                                                                                                                                                                       69736 caksakarictacariacistakciscriaastsasariactscsassasassassas 69677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rcracciadecaarcagaacarcececcacciceceaaaagreecreagaa 69617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69436 GAGGACAACAACACGAAGCTAACCAACGTTCTCTTGTCAGATCTCCCAGATACTCT 69377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69556 ACAACATCCGGCTTCCTTCAAAGCTTGCTGGCCGAAACCCCAAAAAACACGAAAATCGACT 69497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69316 TTCAAGAACGGTCACCAAGAGAACTTCTCTAAGTTATGGTCACATGATCTGGATATTG 69257
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Wolinella succinogenes
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
                                                                                                                                                                              AAGGTCTCAGTCATAAGTTTTTACCAGGAACAATGACAGGACTTGGAGCGTCCGGTT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTTGTCGAGGATGTAGACCTTCTGAAACTCTTCTGCGCGTAAGCAACGGTTATACAGGA 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAACCTTC------AGCTTGCGGTGGAAAAACACAAATGGCCTGAAATTCCTC 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 GTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCGAATAATTC 460
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      (387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 AAGTACTICAIGCTGTIGGTCTIGAGTCGTICGAGGAAAAGCCAGTITITGAACTCTG
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                                                                                                                                      Gaps
glycosyl transferase GlgA TR:Q9X9U5 (EMBL:AJ243803)
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Submitted (15-MAY-2003) Max-Plank Institut for Developmental
Biology, Spemannstr. 35, 72076 Tuebingen, GERMANY
Location/Qualifiers
                                                                                                                            12;
                                                                   Length 341553;
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                                                            15.1%; Score 91.8; DB 1; Length 3 49.2%; Pred. No. 1.9e-16; ive 0; Mismatches 277; Indels
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                                                                                                                        Conservative
                                                                                       il Similarity
280; Conserva
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                                                            Query Match
Best Local S
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/transl_table=11
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/product="cyta PROTEIN PRECURSOR"
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/db_xref="G1:3482182"
/db_xref="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCMORSMIGY PLPAEGKEMKAFLAYIHWLGGGI PVGAKI EGRSLKTYDRKMVQQNAAD VKNGAEVYARDCASCHGAEGEGLRRESKDGKPAGYEFPPLWGSDDTYNTGAGMYRTLK AADFIKSTMPKGAPTLSDKDAYDVAAFINDYSHYRTVKLNRQNDFVDPKVRVFDHDQPGPYGPEGSYI FPDEGKTQMDYKVGPYKGI I KQKPAAK"
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                                                                                                                                                                                protein id="CAE09182.1"
db xref="GI:34482181"
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/ product= PUTATIVE CHOLINE TRANSPORTER"
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LLISSPLIHPEIPEIGTHAPLLIIAFVIFYXHIPNLVRLFQGKEGRVV"
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pdyatyyleyvpsSlvvelkaiklyinsFrdrhVshedsanbiydllykklsFyely
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trans1_table=11
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fprotein_id="CAE09179_1"
db_xref="GI:34482178"
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complement (8279. .9136)
/locus_tag="WS0007"
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complement(9299. .9790)
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'db_xref="GI:34482176"
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897. .6220
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                                                                                                                                                                                               155 AACCAAGTICCGGACAGAICCTIGICGAGGAIGTAGACCTICTGAAACTCTTACGCGTA
                                             Gaps
                                             ö
Length 347961;
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us-09-868-338-7_copy_1117_1725.rge

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//Ogene="POP05"
//Oce="60 ao, similar to gp:AF143819 l transposase-like
protein from Escherichia coli (402 aa); 38% identity in 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="MNIIEISNLNKKYFDKVIFKDFSLSIKKGEMIAISGRSGCGKST
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ILADEPTGSLDEENNIIISLLKELNESGKTIIIVTHDNYVAKQADRIIFL"
                                                                                                                                                                                                                                                                                                                                                                  /note="83 aa, similar to pir:T14710 probable transposase
from Yersinia pestis (402 aa); 44% identity in 50 aa
overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4588. .4746
/gene="PCP06"
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from Yersinia pestis (105 aa); 56% identity in 50 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (5169. .5804)
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/function="ATP-binding protein"
/function="AII aa, similar to gp:AP001508 4 ABC transporter
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49% identity in 214 aa overlap"
                                                   no significant homology"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    producT="probable ABC transporter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                runcated"
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SKODNLLAFALERIEDKYDYCLIDCPPALNNITVNALCASDBYLVPIKIDKFALDGLE
YLLDSIEBIKDERPRILNEKGCFITMDSSTTVNKVIKQELKSVLGERMFNTSIHQNIK
VVESTFEECPVVFSSKKARARAGLNYKDLSKEIF
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KIRDIIANDINLSATQVGRYERINNKLIPELKAVIEQGNLTIANASEFSSLSEENQRV
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TKERAKENNIEKQRIDELSKLKERSNNEVDINTKTENFVLVQNIKLIDNSFKNIKSQI
NYMKKENVKVAEETKAKEFLEKYQKEISDLLKKL"
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Eknfyeivdieslaediklnginhnlyvrkldndmyelisgerrytalsklynegnke
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protein from Lactococcus lactis subsplactis (242 aa); 30%
identity in 266 aa overlap
                                                                                                                                                                                          Shimizu,T., Ohtani,K., Hirakawa,H., Ohshima,K., Yamashita,A., Shiba,T., Ogasawara,N., Hattori,M., Kuhara,S. and Hayashi,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-APR-2001) Tohru Shimizu, Institute of Basic Medical Sciences, University of Tukuba, Department of Microbiology; 1-1-1 Tennohdai, Tsukuba, Ibaraki 305-8575, Japan (E-mail:tshimizu@md.tsukuba.ac.jp, Tel:81-298-53-3354, Fax:81-298-53-3354)
                                                                   Clostridium perfringens str. 13
Clostridium perfringens str. 13
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="250 aa, similar to pir:140444 Spo0A activation inhibitor soj from Bacillus subtilis (253 aa); 37% identity in 250 aa overlap
                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99 (2), 996-1001 (2002)
21664373
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AP003515.1 GI:15076712
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gene="parB"
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gene="parB"
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Shimizu, T.
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/gene="soj"
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ACCESSION
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301439 bp DNA linear BCT 06-FEB-2003 Clostridium tetani BBB, section 8 of 10 of the complete genome. AE015943 AE015927 AE015943.1 GI:28204047
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5558 ATAAGTTACTTATTTCAAAATTTTGCCTTGGTAGAAGAAAGTGAAGAAACTGTAGAGAAATTTA 5499
                                                                                                                                                                                                                                                                                                              5379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5258 AAAGAACTTAATGAAAGTGGAAAAACAATAATTATCGTGACTCATGATAATTATGTTGCA 5199
                                                                                                                                                                             5498 AGACTTGCGATTAAGCACACAATTAAAATACGAAAAAGATTGAAGAAGAATAATAAGA 5439
                                                                                                            342
                                                                                                                                                                                                                                                                                                                                                                                   462
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Submitted (31-OCT-2002) Goettingen Genomics Laboratory, Institute
Submitted (31-OCT-2002) Goettingen Genomics Laboratory, Institute
Of Microbiology abenetics, Georg-August University,
Grisebachstr. 8, Goettingen 37077, Germany
Location/Qualifiers
1. 3014261
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Bruggemann, H., Baumer, S., Fricke, W.F., Wiezer, A., Liesegang, H., Gottschall, C., Herzberg, C., Martinez-Arias, R., Merkl, R., Henne, A. and Gottschalk, G.
The genome sequence of Clostridium tetani, the causative agent of tetanus disease.
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Decker, I., Herzberg, C., Martinez-Arias, R., Merkl, R., Henne, A. and
Gottschalk, G.
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Clostridium tetani B88
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium:
                                                                                                                                                                                                                                                                                                           GGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCGGAATAATTCTG
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                                                                                                        ----AAACACAAATGGCCTGAAATTCCTCAA
                                                                                                                                                                                                                                                 343 GTACTICAIGCIGITGGICTICAGICGITCGAGGAAAAGCCAGITITIGAACTCTCTGGI
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:. .778
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22457253
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                                                                                                                   CAGCTTGCGGTGGAA---
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ISIIILANTSIY FRONNKKIIVKKAHOYRLIRYRNNYFINNLITWTCPLAIASLITKÄ
INIIYFTLIVVIELVYFIINNLISLAKKHLKVIKVIKGEY"
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                                                                                                                                                       /note="720 aa, similar to gp:AP001508_3 BH0280 gene
product from Bacillus halodurans (713 aa); 23% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MKKKVALILITIIIIEPEGVYSVRNHTEPMKLKVLQGNLENF
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LETIQIERROLLDGLIEDLKSBSIIVQKRVMGDSSQYNTETLKIILVVCFIGLIFMIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YOULGSYKKIGIOKLIGHSTFVMLKBELLEURIEUTVMLVVTVLLVFFNFKTFNSLF
WKFMLELICIYSIMIIFTIVSVIIPYIYVSKITLSNIIKNKRPVKSIIILMSIVKVIL
ASIILIFFSNALDDLSSIGKGYEKNYKVWEETKQYYILPELGFNDESIQSFSIEEMEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mkrnkLiktflasLLLvGsLGTTALAYTHSSDKFBAASLPGLFS
QAQSSKFYGGGQKHRATARVKVGTTLYBAKDIKDAKLTAHAQTKYYKGVTEWNSYYAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="77 aa, similar to probable transposase from fersinia pestis plasmid pWT1 (402 aa); 25% identity in 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5678 AGTACCCTTTTAAATATGATAGGCTTGATAGAAAATTTGATTCAGGAGAAATAATTATT 5619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5618 GACGGTGTAAAAAATATAAAAATAAGCAAATTAGCAAATAAGTTTTTAAGGGAAAAG 5559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAATTCAACCTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGATAGAAATCAATGACCTCAAGAAATCTTTTGGCGTTCGGATCTTATGGCAAGGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTATAGAAATTTCAAATTTAAATAAAAGTATTTTGATAAGGTAATATTTAAGGATTTT
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                                                                                                                                                                                                                                                            'codon_start=1
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'trans] table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 83.8; DB 1; Length 5
Pred. No. 3.7e-14;
0; Mismatches 307; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="103 aa, no significant homology'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transI_table=11
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/gene="PCP08"
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0
                                                                                                                                                                                                                               61 aa overlap"
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trans1 table=
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gene="PCP10"
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Best Local S
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Matches
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5825..6607.
5825..6607.
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5825..6667
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/ prodein id="AA036496.1"
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codon_start=1
transl_table=11
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transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKSIQDLFKEII"
                                                                                                                                                                                                                                                                    5132. .5824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trans]
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VISKISTIMYKDNLNIGTMKLYRNSKGSMATWALETDNVIPQATIEKLKKIPEIHSIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /trānslation="MVYNLKYSLYMEWLIMEKEVKAILDNVSVFSNIYDMVRIIDPIA
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KKLOVVFKDNVPKADGSWEFTIESSHHLGDLERICDNVAFINKGTISYNNIDDMKHNI
LSLEDMFIXSVEEDEHNEKILA"
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CDS

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identified by sequence similarity; putative"
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TSLRYAVQLLAPAXEFAKMRNSGKVELEDVERAASIFADVSGSSAYLKKWEEKMLGM"
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Klenk,H.P., Clayton,R.J., Tomb,J.-F., White,O., Nelson,K.E., Kelmuk,H.P., Clayton,R.J., Gwinn,M., Hickey,E.K., Peterson,J.D., Richardson,D.L., Kerlavage,A.R., Graham,D.E., Kyrpides,N.C., Richardson,D.L., Kerlavage,A.R., Graham,D.E., Kyrpides,N.C., Richardson,D.L., Rerlavage,A.R., Graham,D.E., Kyrpides,N.C., Fleischmann,R.D., Quackenbush,J., Lee,N.H., Sutton,G.G., Gill,S., Kirkness,E.F., Dougherty,B.A., McKenney,K., Addms,M.D., Loftus,B., Peterson,S., Reich,C.I., McNeil,L.K., Badgas,J.H., Glodek,A., Lou,L., Overbeek,R., Gocayne,J.D., Weidman,J.F., McDonald,L., Utterback,T., Cotton,M.D., Spriggs,T., Artiach,P., Kaine,B.P., Sykes,S.M., Sadow,P.W., D'Andrea,K.P., Bowman,C., Fujii,C., Garland,S.A., Mason,T.M., Olsen,G.J., Fraser,C.M., Smith,H.O., Woese,C.R. and Venter,J.C.

Direct Submission

Submitted (15-DBC-1997) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA

Medical Center Dr, Rockville, MD 20850, USA

In order to show the genes in ascending order on the genome, the original version and the opposite strand is shown from the original version and the opposite strand is shown from the original version.

In coation/Qualifiers

Location/Qualifiers

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Archaeoglobus fulgidus DSM 4304"
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1751. .2107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125168 GATGGTGATGAAATATAAAATAAATTCATCGAAATCAAATAAGATATTAAGAAAAA 125109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125288 TCACTAGATATACAAGATGGAGAACTCCTAGCTGTAACTGGAGCAAGTGGAAGTGGAAAA 125229
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DSM 4304 section 130 of 172 of the complete
                                                                                                                     IAKIDIKLITKKOGKYIVSDKTKUDVTSKI IMMOGKTKKVNYESDKDLEKKLNSYHKVA
LDDANOI IGELKGGNLVPEDEVKGI PTSQIQETPMINLINEVQMYYTKANVSAAAFR
SNANNKQGKI KKSDASLI YKPDNTLYLLEVTGKQLKDYMSASSYYNYYKGFULTVSF
BDDRGYNYDMFSGYKYEI DIS SKE PGNR I TNIRRMDNSLVKDTETLKLI VNNYRASSH
LLNPNSGI FKDGSLEVLI EKDALDGTPI RDI LIGRYI KEVKKGVITPQMNNWLSGNN
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VYHNSEGEEYGNKNSSAVSLANACPELVAIVAAHEHKAVDGATYNNVLLVENKNLAQT
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Archaeoglobus fulgidus DSM 4304
Archaeoglobus rechaeocta, Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus,
1 (bases 1 to 10575)
Klenk, H.P., Clayton, R.A., Tomb, J., White, O., Nelson, K.E.,
Ketchum, K.A., Dodson, R.J., Gwinn, M., Hickey, B.K., Peterson, J.D.,
Richardson, D.L., Kerlavage, A.R., Graham, D.E., Kyrpides, N.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AIGATAGAAATCAATGACCTCAAGAAATCTTTTGGCGTTCGGATCTTATGGCAAGGTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Score 83.6; DB 1;
Pred. No. 6.6e-14;
0; Mismatches 284;
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KEYWORDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPAFFILUSIFMTYALLSRIFREQUENTAVMRALGFTRNEIMLHYLOYPLLMGFFAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAAAATCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5526 GGTAAGACGATGCTGAACATAATTGGGGGAATTGACAGGCCAACAAGGGAAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5586 ATTITICATGGTAAGGATATCACGAATTACAATGAAGACAGGCTCACCATGCACGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 AATACGGIGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6466 GGGATAAATCTTGAAATAGAGCGGGGAGAGTTCATGGTCGTTCTGGGCCCCTCAGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITGICGAGGATGTAGACCTICTGAAACTCTTACGCGTAAGCAACGGTTATACAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6646 AATAACGITGGCTTCTTTTTCAGTTCTTCAACCTCATTCCAACATTAACTGCAAGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACCTTCAGCTTGCGGTGGAAAAACACAAATGGCC----TGAAATTCCTCAAGTACTTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCGAATAATTCTGGCTGATGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="hypothetical protein; identified by GeneMark;
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Pred. No. 4.3e-14;
0; Mismatches 255; Indels
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7031. .9406
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al Similarity 49.1%;
249; Conservative
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ISIEATI IAVVETTASAI AVIDELKEVPAGIAR PREPEAGKKI LLERRATETURKETES
TKKVTARNI ERYKQRELMTVI GIAA CTGLMI TGFGI KSGVI GAVEKGETES
TKKVTARNI ERYKQRELMTVI GIAA CTGLMI TGFGI KSGVI GAVEKQE SSVYKYDMĢT
TINNI DIDSEKKEI KDKVNORDSNI KSVLPFY VSKATVVREDNNN BDINI VV VPEKKARQU
NEYI ELE-NDSGELKELSDGVI VTEKLAKLMNKKGDVFNI TVDNRI II RVKI FPI TKHY
I QHYI YMSPKYYKKVTGENAQFNAFYGLLKSKSSAENTTSKI I GGIKNI GAVSFKNN
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Childress, D., Zeng, Q. and Smith, D.R.
Direct Sibmission.
Submitted (24-JUL-2001) GTC Sequencing Center Production,
Finishing, and Bioinformatics teams, Genome Therapeutics Corp., 100
Beaver Street, Walcham, MA 02453-8443, USA
Location/Qualifiers
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472 CCAACCGGAGCTCTAGATTTAACAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTC 531
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Nolling, J., Breton, G., Omelchenko, M.V., Markarova, K.S., Zeng, Q.,
Nolling, J., Breton, G., Omelchenko, M.V., Markarova, K.S., Zeng, Q.,
Solbson, R., Lee, H.M., Dubois, J., Qiu, D., Hitti, J., Wolf, Y.I.,
Tatusov, R.L., Sabathe, F.,
Daly, M.J., Bennett, G.N., Koonin, E.V. and Smith, D.R.
Genome sequence and comparative analysis of the solvent-producing
J. Bacterium Clostridium acetobutylicum
J. Bacterium (193 (16), 4823-4838 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium acetobutylicum
Clostridium acetobutylicum
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
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/protein_id="AAK78798.1"
/db_xref="GI:15023713"
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/ Organism="Clostridium acetobutylicum"

/ Acid type="genomic DNA"

/ Strain="ATCC 824"

/ db_xref="ATCC:824"

/ db_xref="taxon:1488"
                                                                                                                                                          6946 AACAGGAAGGAGGGAATAACCTTTGTT 6972
                                                                                                     532 GCCGACAAAGGCGCCACCGTTGTTGTT 558
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/gene="CAC0822"
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/gene="CAC0821"
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/gene="CAC0823"
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/transl_table=:
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Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
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/gene="cobN"
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/gene="cobN"
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                                                                                                                          /product = "Fructose bisphosphate aldolase"
/product = "Fructose bisphosphate aldolase"
/protein id="AAK78803.1"
/protein id="AAK78803.1"
/brotein id="Good state 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/codon_start=1
/product="Hypothetical protein"
/protein_id="AAK78804.1"
/db_xref="GI:15023719"
/translation="MKTIKYLKSNLPSFFKKLTILSPLFIFLLTGCNLNSKSVTLSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISALENTYKKNSIEGSTSTSYIKVENKKYAVVHSRVRADNSIIDSDTLVVINGDYQYE
FREBASDSYKKYNYRDMIMMRFKILKYYKKASPNPOTKNINIKDLNGSWGIKNSNY
TDKRLVLNNDSSFKYYYKQSADEKNVITGTYIYSKDNILTFTLSKVINDGQEVPITASK
VIKFKVTYLKGNTIHLTNTSSLSSYSYVRLDN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (9320. .10246)
/gene="CAC0828"
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1 (Dases 1 to 12929)
Deppenmeier, U., Johnan, A., Hartsch, T., Merkl, R., Schmitz, R.A.,
Martinez-Arias, R., Henne, A., Wiezer, A., Baeumer, S., Jacobi, C.,
Brueggemann, H., Lienard, T., Christmann, A., Boemecke, M., Steckel, S.,
Bhattacharyva, A., Lykidis, A., Overbeek, R., Klenk, H.-P.,
The genome of Merhanosarcha mazel: evidence for lateral gene
transfer between bacteria and archaea
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Deppenmeier,U., Ohann,A., Hartsch,T., Merkl,R., Schmitz,R.A.,
Martinez-Arias,R., Henne,A., Wiecer,A., Baeumer,S., Jacobi,C.,
Brueggemann,H., Lienard,T., Christmann,A., Boemecke,M., Steckel,S.,
Bhattacharyva,A., Lykidis,A., Overbeek,R., Klenk,H.-P.,
Gunsalus,R.P., Fritz,H.-J. and Gottschalk,G.
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EATNPDLISDDMWNKVYQTYMADQELSDWVKQNNPYAYQSWTARMLETARKGSWDASD
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SRTBEHKSROGHOTSVAEKAKQTAKSNTEEPVSNQTVQNSDAGYGVDSPEPAPBYRQS
ADPDVVEGYBMQKESSEGAESGGMSFSGADIIGTLFVVAVVGGIYLGFRKKKM"
COMDIEMENT (4905. .5342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-AUG-2001) Goettingen Genomics Laboratory, Institute for Microbiology and Genetics, Grisebachstrasse 8, Goettingen
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/strāin="Goel"
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1. .12929
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9908 réadgricáaradcaaakcaaggacricgrirgricagarirrraaggaarrigagcicagaa 9849
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50.8%;
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Best Local (
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LipkehGkhvytpykrcsekalrislkpdalpqdsrhtalpakagtaspeeekefq
Ashdaksqrilempeeelfrvsevniepperaliyptvicskcgegfmeplgrvknge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQIKKLRDDSLVFRTEDSYFLSPLGIAVAERMHAMMRVLNVFSRNYDYMADHAVBCL;
PREXRIGADDENCIPSEPDPWHLEPERBEVELTYNSRKIKGISAIFPPLYPSLFLS
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KSFMVAAETFKFSPSTILGIPIEIERSTDEVVDPSVIAAELPHVQVKNPAFDFTPSEY
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IFQHYNLIPTLSALENVELANGSKERKERAKSLLEDIGLEDRILSPELSVER
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                                                                                                                                                                                                        /product="tungsten formylmethanofuran dehydrogenase,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="conserved protein"
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                                                                              complement (5335. .5853)
                                                                                                                       complement (5335, .5853)
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10268 CATAGGCACACTTGAAAAAGCCACTGACGGAAAAATAATTCTTGACGGGACAGACCTTAC 10209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10088 ITCAAGAATGCAAAAAAAAGAGAGAAAAAGAGAAAATCCCTTCTTGAAGACCTGGG 10029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypochetical binding protein of ABC transporter"
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SQQRVSIARALANKPALILADEPTGEVDSKTRDSVVQIFKELSQKGQTILVVTHDPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKGTSTLSPCELEVQARQSFNIFSVITISSGLLAAIIGGLCVMNYMLMSVAERTREFG
ILKALGAETKDILLIJLGEASLMGLLGGILGIIVGIGAVQIMNAWLATTRIVLFLITP
RLLIIAMLFALLIGALSGLYPAYRASKMSPMEALKHA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTINWPLLLEKDRSTTALLKYHSTBELTTYKMSEFWAEEKVELLOSDINVDEYGASV
TVTGRSQVPFNGIVRVVLTPBEGDVRVFEETADILTAGKEDTVGIIWGGVPRGDXNVK
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KKO"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KQILGVPPEKSSVALNPVQLKAGRFLDPGDSYSVVVGNNIKREVNLEIGSKFEIHDKY
FTVVGILDYTGSIFDNAVIIPLETAQDLYSVGNSVSYIFAVPDDRVDAEMLSKRIELS
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DQEISKVFFWELEEDFGKDRDSYTAQLFVKEGNQILETQKTSFSYRNFHLSNLKVVDF
SADSEKASFLIDLVSSANLRLVQMPEPGIVDFDLKLLSGKDIIYSESLKNVPVTDAYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10028 GCTGGAAGACCGGCTCAATCATAAACCTACGGAGCTCTCAGGTGGAGAACAGCAAAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9968 TTCTATTGCAAGGGCTCTGGCAAATAAACCTGCCCTGATTCTGGCTGACGAGCCTACAGG
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Pred. No. 9.3e-14;
0; Mismatches 235; Indels 1
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                                                                                    complement (10455. .11570)
                                                                                                                                                               complement (10455. .11570)
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                                            AKECSRVLRITDGMIKDH"
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complement (6307. 7917)
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/ outplement (6307. 7917)
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                                                                                                                                                                                                                                                                         PIWSAGMDT TEAKYAIAIARQGGIGYVHKANSIEQQAEEIEKVKRSESGVIIDPFYL
TPDHQVFAAEHLMGKYRISGYPIVNNEKERKLVGILINNDDARISDYSTVIKDYMTKE
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VAGNVATAEGARALFEVGVDIVKVGIGPGSICTTRVVAGVGVPQIIAIYDCATVAREF
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                                 gene="guaB"
note="similar to inosine-monophosphate dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="similar to beta-glucosidase"
codon start=1
trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="similar to unknown protein"

codon start=1

fransī table=11

protein id="CAC98127.1"

db xref="GI:16415443"

db_xref="SWISS-PROT:Q926X8"
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8435. .9889
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CDS
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L. Science 294 (5543), 849-852 (2001)
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/ FORCE = 1.

/ FORCE = 1.

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SODSRIOOFILEQSEMDDERKQNESKREKREVERICKTIAKYLTGSSADGKVKUMRFEELST

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YGLMKDASGXDLFEKLREYRRELAAKHKVPPYIIFSDELLREMCAYMPQTEDALLEVK
                                                                                                                                                                                           ALS96174. 96208 bp DNA linear BCT 06-JUN-2002 Listeria innocua Clip11262 complete genome, segment 12/12. ALS96174 ALS92022
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Direct Submission
Submission
Submitted (09-001). 2001) Glaser P., Institut Pasteur, Genomique des
Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris
Cedex 15, FRANCE
E-mail: pglaseregesteur.fr
E-mail: 1991aseregesteur.fr
Phone: +33 (0)1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.
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Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
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19575 Traderrrratarrecaaarraterrreareeaaareaaacaererraeaaaerra
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0.500.001 to 1.249.980-seq 4035: 1.200.001 to
1.549.980-seq 4036: 1.500.001 to 1.849.980-seq 4037:
1.800.001 to 2.149.980-seq 4038: 2.100.001 to
2.700.001 to 3.049.980"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19275 GGTAAGACTATCGTTTGTGTCACGCATGACCCGGAAATATCAGGAAAAGCAGATCGGGTC 19216
                     TCGACTITGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTC
                                                        19689 ACAACGCTGCTAAATGTTATCGCACACCTAGATTCAAAAGATAGTGGGCAAGTTATTATT
                                                                                                                                         AACGAGATGGAATATCAGA-----CGAAAAAAGAGGTTATGACTCTAAAAAAGAGGTG
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                                                                                                  GAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAAAATACG
                                                                                                                                                                                   CAGCTTGCGGTGGAAAAACACAAATGGCCTGAAATTCCTCAAGTACTTCATGCTGTTGGT
                                                                                                                                                                                                                                                                                                                                                  361 CTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGAACT
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Patent: WO 0228891-A 4040 11-APR-2002;
INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE
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Pred. No. 5e-13;
0; Mismatches 312;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to xylose operon regulatory protein and to jlucose kinase"

codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGATTGAATTAGTTAATGTCAGTAAAAGATACAAGATAAATTGATTTTGGAAAAAGTC
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                                                                                                                                                               note="similar to PTS cellobiose-specific enzyme IIB"

codon start=1

cransl_table=11

protein id="CAC98130.1"

db_xref="GI:16415446"
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Pred. No. 3.7e-13;
0; Mismatches 312; Indels 6;
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/12497, 10512
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/gene="11n2906"
110258. 10263
/gene="11n2906"
10271. 11623
/gene="11n2906"
                                                                                                                          9935. .10237
/gene="lin2905"
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/gene="lin2907"
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/gene="lin2908"
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Matches 28
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346125 ACAACGCTGCTAAATGTTATCGAACACCTAGATTCAAAAGATAGTGGGGAAGTTATTATT 346184
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/db_rare="taxon:1642"
/note="seq 9 splitted in 3 part.~seq 9: 1 to 349980-seq
4027: 300001 to 649980~seq 4028: 600001 to 684707"
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                                        1 ATGATAGAAATCAATGACCTCAAGAAATCTTTTGGCGTTCGGATCTTATGGCAAGGTCTC
                                                                               346005 ATGATTGAATTAGTTAATGTCAGTAAAAAGATACAAGATAAATTGATTTTGGAAAAAGTC
                                                                                                                 TCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTC
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Listeria innocua
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria
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    Mismatches 312; Indels
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Listeria inocua, genome and applications
Patent: WO 0228891-A 4027 11.APR-2002;
INSTITUT PASTEUR (FR), CENTRE NATIONAL DE
SCIENTIFIQUE (CRRS) (FR)
Location/Qualifiers
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Sequence 4027 from Patent WO0228891.
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AX417036.1 GI:21449646
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    284; Conservative
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AUTHORS
TITLE
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AX417036
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seq 9 from 1 to 349980~seq 4027 = old seq 9 from 300000 to
649980~seq 4028 = old seq 9 from 600000 to 684707"
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                                                                                                       TCTCTTTCTATTGGAGCTGGCGAATTTATTGCAGTCGTCGGCGAGAGTGCTAGTGGGAG
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                                                                                                                                                                                      234689 ACAACGCTGCTAAATGTTATCGGACACCTAGATTCAAAAGATAGTGGGCAAGTTATTATT
                                                                                                                                                                                                                            GAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAAAATACG
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                                                                        ATGATAGAAATCAATGACCTCAAGAAATCTTTTGGCGTTCGGATCTTATGGCAAGGTCTC
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Listeria innocua
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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Pred. No. 5.1e-13;
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Listeria inocua, genome and applications
Patent: WO 0228891-A 9 11-APR-2002;
INSTITUT PASTEUR (FR.), CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR.)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Sequence 9 from Patent WO0228891.
AX413018
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Best Local Similarity
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AX413018
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TITLE
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FRAMPERCYAVFACHERFYGYAGCSLAGCQLVBFAILMINFQTLATKARLKSVIGDDF
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AATFFAIEIIMLGKTEYRALIPALVGSYVAGNTSSSIGLEFREFSFAINTNHIDBLVLL
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Jouy en Josas 78352, France
Location/Qualifiers
1. .11551
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                           FEATURES
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Bolotin,A., Wincker,P., Mauger,S., Jaillon,O., Malarme,K.,
Weissenbach,J., Ehrlich,S.D. and Sorokin,A.
Direct Submission
Submitted (09-JAN-2001) INRA, Genetique Microbienne, Domaine de
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Lattaces I to 11551)

Bolotin, A., Wincker, P., Mauger, S., Jaillon, O., Malarme, K., Weissenbach, J., Ehrlich, S.D. and Sorokin, A.

The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL403

Genome Res. 11 (5), 731-753 (2001)
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                                Indels
    Pred. No. 5.1e-13;
0; Mismatches 312;
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AE006342 AE005176
AE006342.1 GI:12724053
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LWHNILLSAAITFATTLLAIVVHFKLKAVDMLGALKSVD"
complement (9331. .10116)
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/note="synonym: L114717"
complement(10117. .11466)
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/note="synonym: L113931"
complement(9331. .10116)
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SHSYVNVVENAPEAGKVVVNKAYTFSKNGKTYVWKVEGKKVKMKEVKTKKVSDRLVEI
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complement(6301. .16446)
/note="ORF9R: high molecular weight, serine-rich protein;
contains cell wall anchor motif for gram-positive cocci
cell surface protein; contains two amino acid repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="ATP-binding cassette transporter-like protein"
protein id="AAB97962.1"

db_xref="GI:2822200"
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/protein_id=AAB97961.1"
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/codon start=1
/transI_table=11
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'product="unknown"
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?151. .2825
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gene="tptD"
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OTAGTİTSMNEDLPTQSKAKKEESTFIEIMDKSKTLİKGSVSEFDREKLSVGQRVDVV
           Streptococcus crista ATP-binding cassette lipoprotein (tptA), ATP-binding cassette lipoprotein (tptA), ATP-binding cassette transporter-like protein (tptB), ATP-binding cassette protein (tptC) and ATP-binding cassette transporter-like protein (tptB) genes, complete cds and unknown genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-APR-1997) Microbiology, University of Pennsylvania, 4010 Locust, Philadelphia, PA 19104-6002, USA
4010 Locust, Philadelphia, PA 19104-6002, USA
4 (bases i to 19841)
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6 (14-MAR-2000) Microbiology, University of Pennsylvania, 5 (base)
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(Codon start=1 /crans]_table=11
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2 (bases 4397 to 19941)
2 Octreia, F.P., Allen, T.W. and DiRienzo, J.M.
High molecular weight serine-rich protein gene (srpA) from Streptococcus crista
                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Correia, F.F. and DiRienzo, J.M.
Direct Submission
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899. .2164
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ABCOGEGS 10738 bp DNA linear BCT 01-JUN-2001 Streptococcus pyogenes MI GAS strain SF370, section 94 of 167 of the complete genome.
ABCOGEGS ABCOGGS ABCOGGS ABCOGGS ABCOGGS ABCOGGS I GI:13622379 Streptococcus.

1 (bases 1 to 10738)
Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S., Olan,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
Complete genome sequence of an M1 strain of Streptococcus pyogenes Droc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001) 2491 2672 CAAGACCAGIGITCAGATCAIGGAGTIGITCAAGCAGTITAACGAACAAGGGAAAACTAI 2731 2492 iralalangaganggeggaggggggtttggalaigcigcgartggicggtchglalagagag 2551 431 2432 CATGCCTAAGCTGACAGCCTGTCAAAATGTTGAACTGCCTCTGACTTACATGAAAGTTCC 372 CGAGGAAAAGCCAGTTTTTGAACTCTTTTGGCGAACAACAACGAACTGCGTTGGCCCG 492 AACAAACAGTGAGGTAGTCATAGAAGCATTGAGAGCACTGGGCGGACAAAGGGGGGCCACGT GATTCCCGACAGACAGTTAAATTCAACCTTCAGCTTGCGGTGGAAAACACAAATGGCC TCCTCAAGTACTTCATGCTGTTGGTCTTGAGTCGTT Streptococcus pyogenes M1 GAS Streptococcus pyogenes M1 GAS Bacteria, Firmicutes; Lactobacillales, Streptococcaceae; 2732 TGTCATTACCCACGAGCC 2752 552 IGITGITGCTACGCACTCGCC 572 330 TGAAAT----270 ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 15 AE006565/c LOCUS DEFINITION TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS gene CDS PEATURES G 상 점 S G S g & δ g g

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Gane="Spy1260"

/note="The N-terminal amino acid sequence of this ORF has been determined from a spot isolated by 2-D gel
electrophoresis from another strain of S. pyogenes. Hogan, D. A. Whitton, M. M. Rogers, J. and R. A. VanBogelen.
2000. Two-dimensional gel electrophoresis map of Streptococcus pyogenes proteins. Unpublished data.; Best Blastp hit = emb[CAAO3877.1] (AJO00042) gls24
                                                                                                                                                gene="SPy1257"
/note="Best Blastp hit = pir||H72342 ABC transporter,
| האידיהלימים שמדונושם (strain MSB8)
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complement(7336..7977)
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/gene="SPy1259"
/note="Best Blastp hit = dbj|BAA83965.1| (AB024564) YHCF
(Bacillus halodurans) >gi|10172996|dbj|BAB04102.1|
(AP001509) transcriptional regulator (GntR family)
[Bacillus halodurans]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Best Blastp hit = dbj|BAB04438.1| (Ap001509) transcriptional regulator (TetR/AcrR family) [Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /producT="conserved hypothetical protein"
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(COMPIEMPRIA (3181. .5817)
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protein [Escherichia coli]"
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hypothetical protein"
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gene

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gene	Query Match Best Local Matches 24	66 6450	126	186	246	306	363	423	483	543
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Search completed: July 30, 2004, 13:27:45 Job time : 3638 secs

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July 30, 2004, 06:49:19; Search time 450 Seconds (without alignments) 5749.228 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Fotal number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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1: geneseq11980s:*

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3: geneseq1200s:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Aaa65395 Brevibact	Continuation (4 of	Continuation (30 o	Continuation (12 o	Aav65222 DNA encod	Abn66720 Streptoco	r	Aas55747 Streptoco	Abn67102 Streptoco	Continuation (10 o	Abx07412 S. pneumo	Aav52169 Streptoco	Continuation (15 o	Abq71073 Listeria	Aca39374 Prokaryot	Acc69145 M. genita	Continuation (6 of	Aat58840 Mycoplasm	Continuation (13 o	Aca46798 Prokaryot	Continuation (7 of	Abg71007 Listeria	Aca42947 Prokaryot
ΙD	AAA65395	ABQ67196_3	ABQ69245_29	ABA90521_11	AAV65222	ABN66720	ABA03041_28	AAS55747	ABN67102	ABN71527 09	ABX07412	AAV52169	ABS56454 14	ABQ71073	ACA39374	ACC69145	AAT58840 5	AAT58840_0	ABA03041_12	ACA46798	ABA90521 06	ABQ71007	ACA42947
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% Query Match	100.0	13.3	13.3	13.2	13.2	13.1	13.0	12.7	12.4	12.4	12.4	12.4	12.4	12.3	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.1	12.0
Score	609	80.8	80.8	80.6	80.4	80	79.2	77.4	75.6	75.6	75.4	75.4	75.4	75	74.6	74.6	74.6	74.6	74.6	74.4	74.4	73.6	73.2
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73.2	73.2	72.8	72.6	72.4	72.4	72.4	72.4	71.8	71.6	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	70.8	70.8	69.8	69.8	
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ALIGNMENTS

Brevibacterium lactofermentum gltBD gene DNA sequence SEQ ID NO:7. Brevibacterium lactofermentum; ABC transporter; breeding; ATPase; corynebacterium; gltBD; L-glutamic acid; ds. Location/Qualifiers
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99WO-JP007079 WO200037647-A1 16-DEC-1999; 29-JUN-2000.

98JP-00360621. (AJIN) AJINOMOTO CO INC. 18-DEC-1998;

Kanno S, Kimura E, Matsui K, Nakamatsu T;

WPI; 2000-452189/39. P-PSDB; AAB12591, AAB12592, AAB12593.

ABC transporter constituent of Brevibacterium lactofermentum, its encoded gene and variants, applicable in breeding Corynebacteria particularly for production of L-glutamic acid.

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of AB069245 from base 2900001 (Listeria innocua DNA sequence #684)
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                                                                                                                                                    ATGATTGAATTAGTTAATGTCAGTAAAAAGATACAAGATAAATTGATTTTGGAAAAAGTC
                                                                                                                                                                                               rerettretarregaeeregeeaarrratrecagregeegegagagregregaag
                                                                                                                                                                                                                                                                                                                              16125 ACAACGCTGCTAAATGTTATCGGACACCTAGATTCAAAAGATAGTGGGCAAGTTATTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCCGACAGGACAGGTTAAATTCAACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCTTGCGGTGGAAAAACACAAATGGCCTGAAATTCCTCAAGTACTTCATGCTGTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16299 TCCATTACAGGTGGGGAAAATCGCAAGCTGATGATAGAGCATTTGGAAGAAGTAGGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46419 GCTATTGTGCGCATTTTACTCAAACCATTTCAACTTTTACTTGCGGACGAACCAACTGGC
                                                                                                          ATGATAGAAATCAATGACCTCAAGAAATCTTTTGGCGTTCGGATCTTATGGCAAGGTCTC
                                                                                                                                                                                                                                                                                    TCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTC
                                                                                                                                                                                                                                                                                                                                                                           GAGGATGTAGACCTTCTGAAACTCTTACGCGTAAGCAACGGTTATACAGGAAAAATACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46359 GATGAGAGCTATTTAGCAAAAAAGTATACCAATTAAGTGGTGGAGAAAAACAACGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGACAAA
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                                                             9
                     Length 110000;
                                                             Indels
                Score 80.8; DB 6;
Pred. No. 8.3e-15;
0; Mismatches 312;
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                                     The present invention describes a protein (I) which can be used to construct an ATP binding cassette (ARC) transporter. ABC transporter DNAs can be used in breeding Corynbacteria particularly for production of L-glutamic acid. The present sequence encodes three ORFs (open reading frames) from the Brevibacterium lactofermentum gltBD gene, which is used in the exemplification of the present invention. (Updated on 15-SEP-2003 to standardise OS field)
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WP ABQ69245_18 1800001 2010000 WP ABQ69245_19 1900001 2010000 WP ABQ69245_20 2000001 2110000 WP ABQ69245_21 2100001 2310000 WP ABQ69245_22 2200001 2310000 WP ABQ69245_24 24 2400001 2510000 WP ABQ69245_24 24 2400001 2510000 WP ABQ69245_26 2600001 2710000 WP ABQ69245_27 2700001 2610000 WP ABQ69245_29 2900001 2710000 WP ABQ69245_29 2900001 3010000	34809 61 34749 1121 34689 1181	34575 TIA 301 CAG 34515 TCC 361 CTF 421 GCG 421 GCG 481 GCT 481 GCT 34335 AAT 541 GGC	CY 601 AT 602 Db 34215 AT 34214 RESULT 4 ABA90521 II CONTINUATION (12 of 24) of ABA90521 from base 1100001 (Genomic sequence of Lactococcus 1 Continuation (12 of 24) of ABA90521 from base 1100001 (Genomic sequence of Lactococcus 1 Continuation (12 of 24) of ABA90521 from base 1100001 WP ABA90521 01 100001 1100000 WP ABA90521 01 100001 1100000 WP ABA90521 01 200001 310000 WP ABA90521 01 200001 310000 WP ABA90521 01 200001 310000 WP ABA90521 03 300001 510000 WP ABA90521 03 300001 510000

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Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
587 CGACTGGAGCCTTGGATTATCAGACGGCAAGCAGGTTTTGAAA 544
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24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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                                                                                           ABN66720 standard; DNA; 711
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(GENO-) INST GENOMIC RES
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Tettelin H;
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                                                               RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                     This DNA sequence encodes a Streptococcus pneumoniae transport protein. The invention provides DNA sequences (AAV65201 to AAV65304) from the Streptococcus pneumoniae genome and corresponding protein sequences (AAAW8065 to AAAW80728). A recombinant host contraining a vector comprising any of the above nucleic acids can be used for the recombinant expression of the protein sequences. The invention also provides a DNA chip having arrayed on it at least 15 base pair fragment of any one or more of these DNA sequences. The DNA chip can be used methods for evaluating gene payrespression in S. pneumoniae and for identifying virulence genes in S. pneumoniae. Antibodies that selectively bind to the above proteins or peptide fragments can be used to treat S. pneumoniae infection. The
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                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae nucleic acid sequences - used in DNA chips for evaluating gene expression, and identification of virulence genes.
                                                                                                                                                                                                      SR;
Skatrud PL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          647 AGCGAGTCTCCATTGCACGCGCGGTAGCCAAAAATCCTAAAATTCTCCTTTGTGATGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       947 GGCAAGTCAACAGTTCTTAACCTTCTTGGGGGAATGGATACCAATGATGAAGGGGAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 CTTGTCGAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 CTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 80.4; DB 2; Length 1010; Pred. No. 9.9e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1010 BP; 285 A; 247 C; 207 G; 271 T; 0 U; 0 Other;
                                                                                                                                                                                                 Dehoff BS, Hoskins JA, Jaskunas
Peery RB, Rockey PK, Rosteck PR,
J, Treadway PJ, Young Bellido ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibodies can also be used to detect S. pneumoniae cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 CAACCGGAGCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 231; Indels
                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 63; 333pp; English.
                                                                                                            97WO-US022578
                                                                                                                                         96US-0036281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 49.8%;
Matches 231; Conservative
                                                                                                                                                                                                                                   Solenberg PJ,
                     Streptococcus pneumoniae
                                                                                                                                                                                                    Burgett SG,
Norris FH,
                                                                                                                                                                     (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                  WPI; 1998-348529/30.
                                                                                                                                                                                                                                                                                 P-PSDB; AAW80648
                                                                                                                                         13-DEC-1996;
                                               W09826072-A1
                                                                                                                                                                                                   Baltz RH,
Mills BJ,
Smith MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes).

(Streptococcus pyogenes), comprising one of 5481 sequences (51), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detectine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125
           οr
New Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 711 BP; 211 A; 130 C; 159 G; 211 T; 0 U; 0 Other;
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Qy 1 ATGATAGAAATCAATGACCTCAAGAAATCTTTTGGCGTTCGGATCTTAIGGCAAGGTCTC 60	ь	OY 121 TCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTC 180 Db 58083 ACACGCTGCTAAATGTTATCGGACACCTAGATTCAAAAGATAGGGGCAAGTTATTATT 58024	OY 181 GAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAAAATACG 240 Db 58023 AACGAGATGCAATATCAGACGAAAAAAAGAGGTTATGACTCTAAAAAAAGAGGTG 57970	Qy 241 GTGGGCTATTTTCAAGATTATGCCTTGATTCCGACAGGACAGTTAAATTCAACCTT 300	OY 301 CAGCTTGCGGTGGAAAACACACAAATGGCCTGAAATTCCTCAAGTACTTCATGCTGTTGGT 360 Db 57909 TCCATTACAGGTGGGAAAATCGCAAGCTGATGATGAGGCATTAGAAGAAGTAGGAATG 57850	OY 361 CTIGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGAACT 420 Db 57849 GATGAGAGCTATTTAGCAAAAAAGTATAACCAATTAAGCGGTGGAGAAAAAACAACGGATT 57790	OY 421 GCGTIGGCCCGGGTACTGCTCAAAAATCCCCGAATAATTCTGGCTGATGAACCGAACCGGA 480	481 GCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGACAAA 57729 AACTTGGATGATAAAAACAAACAAAAATCATTGAATTATTTTTAGCCTTGAAAAAGCAA	Cy 541 GGCGCCATTGTTGTTGTTGTTGTTGTCGCCCCTCTTCCGAGATCAGGATACCGTT 600 Db 57669 GGTAAGACTATCGTTTGTGTTACGCATGACCCAGAAATACTGCAAAAGCAGATCGAATC 57610	57609 AT	RESULT 8 AASS5747 TD AASS5747	AAS55747;	AA DT 13-FEB-2002 (first entry) yy	DE Streptococcus pneumoniae DNA for cellular proliferation protein #318. XX	\vec{x} Antisense, ds, prokaryotic cellular proliferation gene, antibiotic, \vec{x} antibacterial, drug design.	AA OS Streptococcus pneumoniae. yy	PN WO200170955-A2. XX	PD 27-SBP-2001. XX	21-MAR-2001;	21-MAR-2000; 23-MAY-2000;	FX 23-07-2000; 2000US-024557F. PR 23-07000; 2000US-024557F. PR 27-NOV-2000; 2000US-025555P. PR 22-DEC-2000; 2000US-0257931P.	16-FEB-2001;
Qy 126 TITGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTCGAGGA 185 Db 156 AGTCCTAATATTTTGGGGGGATGGAACAGTAGATGAGAGAGTAAGTA	24	Qy 246 CTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAATTCAACCTTCAGCT 305 Db 276 TTTCGTTTTTCAATTTTATAATTTGGTTCCTAATTTGACAGCTAAAGAAAAGTTGAATT 335	Qy 306 TGCGGTGGAAAAACACAAAATGGCCTGAAATTCCTCAAGTACTTCATGCTGTGT 362. Db 336 AGCAGTTGAAATTGTAGCAGATGCTTTAGATCCTGTGACCATTTAAAGGAAGTAGGACT 395	Qy 363 TGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACAACTGC 422	OY 423 GTIGGCCCGGGTACTGCTCAAAAATCCCCGAATAATTGTGGCTGATGAACCAACC	QY 483 TCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGACAAAGG 542	Qy 543 CGCCACCGTTGTT 558 Db 576 GGGACCACGGTAGTT 591	SULT 7 403041_28/c ntinuation (29 of 30) of ABA03041 from base 280000	t into 30 fragments LOCUS ABA03041 Acces Name Begin End 00 1 100001 210000	ABA03041_03 300001 ABA03041_04 400001 ABA03041_05 500001	ABA03041 06 600001 ABA03041 07 700001 ABA03041 09 800001 ABA03041 09 900001	ABA03041_10 100001 1 ABA03041_11 1100001	ABA03041_12 1200001 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2	ABA03041_15 1500001 ABA03041_16 1600001	ABA03041_17 1700001 ABA03041_18 1800001	ABA03041 19 1900001 ABA03041 20 2000001 ABA03041 21 2100001	ABA03041_22 2200001 ABA03041_23 2300001	ABA03041 24 240001 3 ABA03041 25 250001	ABA03041_26 2600001 3	ABA03041_28 2800001 3 ABA03041_29 2900001	Query Match 13.0%; Score 79.2; DB 6; Length 110000; Best Local Similarity 47.0%; Pred. No. 2.8e-14; Matches 283; Conservative 0; Mismatches 313; Indels 6; Gaps 1;	-

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WPI; 2001-611495/70.
P-PSDB; AAU37888.
     Haselbeck R,
Yamamoto RT,
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RESULT 9

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Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antinflammatory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                                               Streptococcus polynucleotide SEQ ID NO 2117.
                                 ABN67102 standard; DNA; 750 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-OCT-2001; 2001WO-GB004789
                                                                                                                                                                                                01-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus agalactiae.
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                                                                                                                     ABN67102;
ABN67102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Eschericia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aseruginosa and Enterococcus faecalis. The invention is also useful for the identification of porential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins or the express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The used to screen compounds in rational drug discovery programmes. The bused to screen compounds in rational drug discovery programmes. The proteins call sequence is also useful to screen for homologous nucleic acids equence encodes an essential prokaryotic of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent electronic format directly from WIPO at collectronic format directly from WIPO at clear wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Gaps
                                                                                                                                                                                                                                                                                                                                                            polynucleotides for the identification and development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.7%; Score 77.4; DB 4; Length 711; Best Local Similarity 50.8%; Pred. No. 8.2e-15; Matches 236; Conservative 0; Mismatches 226; Indels 3
                                                                                                                     Ohlsen KL, Zyskind JW, Wall D, Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                     antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 9384; 511pp; English
                                              (ELIT-) ELITRA PHARM INC
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABM66044-ABM71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by treptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is are used to detect Streptococcus in a composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be mingitis. Nucleic scid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromococcus and antipolicity and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contractor and contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 caagacgricgatrtraaagrigaacaaggggaarricarrictarragggagagricregr
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                                                                                                                                                                                                                                                                                                                                                                                                     Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3.3e-14;
0; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                     Masignani V, Margarit Y RosI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 3364; 4525pp; English.
27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                   (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 48.3
Matches 259; Conservative
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P-PSDB; ABP26471.
                                                                                                                                                                                                                                                                                                                                                                                                           Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
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51908 TIGARAPATCITIGETITICG TITICAGACTICAACCTITIGGATACTCICTCTGTAAGA 51967
                                                                         51968 GATAATATCTATCTTCCTTTAGTTCTTGATCGTAAACGTTACAAAGAAATGGATCATCGT 52027
                                                                                                                                                                                            52148 ATTTTATTAGCAGATGAACCAACAGCAGCGTTAGATTACCGTAATTCAGAAGACTTGCTG 52207
                                                                                                      334 ATTCCTCAAGTACTTCATGCTGTTGGTCTTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAA 393
                                                                                                                                                                                                                        -----AAAAACACAAAATGGCCTGAA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media cear infection.
                                                                                                                                                                                                                                                                                                               52208 AATTTATTTGAAACTATTAACTTGGATGGACAAACTATTTTGATGGTAACCCATTC 52263
                                                                                                                                  52028 TIGICAGAATIAICTICICATCIGAGAATIGAIGACTIATIAGAIAAGAGACCTITCGAG
                                                                                                                                                                CICICIGGIGGCGAACAACAACGAACIGCGIIGGCCCGGGTACIGCICAAAAAICCCCGGA
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                                                                                                                                                                                                                                                                                  514 GAAGCATTGAGAGCACTCGCCGACAAAGGCGCCACCGTTGTTGTTGCTACGCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene, ds; bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant;

    S. pneumoniae type 4 strain coding region #1700.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      auditory; respiratory; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae; type 4 strain.
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                                               TICAACCIICAGCIIGCGGIGG-
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(GENO-) INST GENOMIC RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-OCT-2003
11-FEB-2003
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                                               292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGGAAAATCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAG 171
                                                                                                                                     372
 GIGATTITAAAIGGGGAAGATATTACGAAAATTAAAGGCAAAATTAGCGAGTITTCGT 252
                                               291
                                                                           312
                                                                                                                                                                 ATTCCTCAAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAA 393
                                                                                                                                                                                            TIGICAGAATTATCTICICATCTGAGAATTGATGACTTATTAGATAAGAGACCTTTCGAG 432
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                                                                                                                                                                                                                                                                                    ATTTTATTAGCAGATGAACCAACAGCGTTAGATTACCGTAATTCAGAAGACTTGCTG 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 ATCCTTGTCGAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 AAAATACGGTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAA 291
                                                                                                       -----AAAAACACAAATGGCCTGAA 333
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                                                                           TIGAAAAATCTIGGITTICGICTTICAGGACTICAACCTITIGGALACTCTCTCTGTAAGA
                                                                                                                                     GATAATATCTATCTTCCTTTAGTTCTTGATCGTAAACGTTACAAAGAAATGGATCATCGT
                                               AAAAATTCCCGACGACTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAA
                                                                                                                                                                                                                           CTCTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAATCCCCGA
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Pred. No. 4.4e-13;
0; Mismatches 259; Indels
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P Sequence split into 22 fragments Lup
P Fragment Name Begin Bn
P ABN71527_00 100001 21
P ABN71527_01 200001 31
P ABN71527_03 300001 41
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800001
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259; Conservative
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ABN71527_20
ABN71527_21
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ABN71527_08
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sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having substantial complementarity define the termin of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and streptococcus pneumoniae bacterium, where one or more genes conding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying identified coding region from the genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the buds. Strendardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 708 BP; 184 A; 134 C; 190 G; 200 T; 0 U; 0 Other;
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185 245 278 306 TCTGACAGCTAAGGAAATGTGGAACTGGCTTCTGAAATTGTGACAGATGCCTTGAATCC 365 425 CACCAATTACCGTAGAATGATGTGGGGTTTTTTCAGTTTTTATAATCTAGTTTCTAA 305 ---TCAAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACT 395 TGGAGCGTCCGGTTCAGGAAAATCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACC TGGTGCTTCAGGTGCAGGCAAGTCAACAGTTCTTAACCTTCTTGGGGGAATGGATACCAA 159 AAGTICCGGACAGATCCTIGICGAGGATGTAGACCTICTGAAACTCTCTACGCGTAAGCA 486 TCTCCTTTGTGATGAACCGACTGGAGCCTTGGATTATCAGACGGCCAAGCAGGTTTTGAA TGATGAAGGGGAAATCTGGATTGATGTTTAATATTGCGGATTATAGTTCCCACCAGCG 219 ACGGTTATACAGGAAAAATACGGTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGA CAGGACAGTTAAATTCAACCTTCAGCTTGCGGTGGAAAAAACACAAAATGGCCTGAAATTCC CTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCCGGGTACTGCTCAAAAATCCCCGAAT TGATCAGGCCTTGACAGATGTAGGTCTGGCTCATCGTCTCAATAACTTTCCAGCCCAGCT 426 TICTGGAGGGAGGACAGGGGGTCTCCATTGCACGCGGGGGAGCCAAAAATCCTAAAAT Gaps 'n Length 708; Score 75.4; DB 7; Length 7 Pred. No. 3.8e-14; 0; Mismatches 206; Indels 12.48; 50.4%; Query Match
Best Local Similarity 50.4°
Matches 212; Conservative 516 A 516 546 A 546 66 126 246 339 396 g ò qq a d g 8 g ò $\dot{\delta}$ ò ò à

The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV5254) recorded on it, or a representative fragment or a sequence at least 984 identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV52134 to AAV5254) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a process comprising of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules to much members, or (b) isolating make, DNA or cDNA produced from an organism, amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines

polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus pneumoniae.

Claim 1; Page 358-371; 1409pp; English.

Computer-readable medium with recorded Streptococcus pneumoniae

Fannon M;

Rosen CA, Barash SC,

Dillon PJ,

Choi GH,

Kunsch CA, C Dougherty BA;

WPI; 1998-272225/24.

HUMA-) HUMAN GENOME

97WO-US019588. 96US-0029960P. SCI INC

30-OCT-1997; 31-OCT-1996;

pneumoniae.

Streptococcus

WO9818931-A2

07-MAY-1998

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21706 BP; 6489 A; 3946 C; 4879 G; 6392 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.4%; Pred. No. 2.2e-13;
Matches 212; Conservative 0; Mismatches 206; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae genome fragment SEQ ID NO:36.
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The present invention relates to mucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to setreen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in antilisteria vaccines. Note: The sequence date for this patent did not form listeria the printed specification, but was obtained in electronic directly from WIPO at ftp. wipo.int.pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9370 ACCACGCTGCTAANGTTATCGGACACCTAGATTCAAAGATAGTAGGAAAGTTATTATT 9311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9490 ATGATTGAATTAGTTAATGTCAGTAAAAGATACAAGATAAATTGATTTTGGAAAANGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides,
                                                                                                                                                                                                                                                     Antibacterial; Listeria; food contamination; mutational analysis;
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                                                                                                                                                                                                                      Listeria monocytogenes 4b contig DNA sequence #1015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; SEQ ID NO 3886; 180pp; French
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                                                                           RESULT 14
ABQ71073/c
ID ABQ71073 standard; DNA; 12278 BP.
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(first entry)
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(CNRS ) CNRS CENT NAT
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516 A 516
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29-AUG-2002
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                                15261 Trichdaaddaaaddaadaadagarcrccarradadacacacagaaccaaaaariccraaaar 15320
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 CTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCGAAT
                                                                                             15321 TCTCCTTTGTGATGAACCGACTGGAGCCTTGGATTATCAGACGGGCAAGCAGGTTTTGAA
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Pred. No. 5.2e-13;
0; Mismatches 206; Indels
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Best Local Similarity 50.4*
...-rhes 212; Conservative
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ABSS6644 14/C
Continuation (15 of 22) oo
WP Sequence split into 22
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GAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAAAATACG
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                                           GIGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAATTCAACCTT
                                                                                                                                                     481 GCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGACAAA
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Xu HH;
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Forsyth R
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prokaryotic essential gene #21031
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Carr GJ,
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2001US-0342923P.
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Trawick JD,
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25-OCT-2001;
08-FEB-2002;
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an extension is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding to polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an openor required for proliferation or the activity of a gene in an openor required for proliferation or that activity as a gene product or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway of the gene product or that has an activity against a biological pathway of a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or ganism acts; (9) manufacturing an antibiotic; (10) profiling the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling the extent or organism; or (13) identifying the target of a compound that inhibits the product is overexpressed or underexpressed; (12) determining the extent or ordifferation of an organism. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids required for cellular proliferation in cells other than S, sureus, S, typhimurium, and surfactoring part of for screening for hamologous nucleic acids required for proliferation in cells other than S, aureus, S, typhimurium, or proceeding and provided and provided and provided and provided and provided and provided and provided and provided and provided and provided and provided and provided and provided and provided and provided and provided and provided and provided
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1e-13;
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Pred. No. 1e-13;
0; Mismatches 209; Indels
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Job time : 455 secs

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Sequence 36, Appl
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Sequence 1259, Ap
Sequence 1763, Ap
Sequence 2763, Ap
Sequence 3320, Ap
Sequence 2762, Ap
Sequence 72, Appl
Sequence 1758, Ap
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Sequence 180, Appli
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Sequence 93, Appl
Sequence 1, Appli
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1: /cgTa_6/ptodata/2/ina/5A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
      version 5.1.6
- 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                             Sequence 1, Appli
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Sequence 1167, Appli
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                          Sequence 1,
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ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STREET: 9410 Key West Avenue
CITY: Maryland
COUNTRY: USA
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US-09-306-417-2
US-09-107-532A-3013
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US-09-107-532A-554
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US-09-134-000C-520
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US-09-023-655-1168
                        US-08-784-649A-1
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US-08-181-471-2
US-09-023-655-1167
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; Sequence 36, Application US/08961527
; Patent No. 6420135
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US-08-961-527-36
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99 IGGAGCGTCCGGTTCAGGAAAATCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACC 158

<u>ب</u>

Length 21706;

12.4%; Score 75.4; DB 4; Similarity 50.4%; Pred. No. 1.7e-15; 12; Conservative 0; Mismatches 206;

Query Match Best Local Simi] Matches 212; (

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US-08-545-528D-1/C
US-08-545-528D-1/C
Sequence 1, Application US/08545528D
Patent No. 6537773
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragments
Patent No. 6537773
TITLE OF INVENTION: Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576792 TATATTITTCAACAATATGGTTTATTGCGTGATCTTGACGTTGATGATAATATTAAGGTT 576733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    576852 ACTAACACCATATGTTGTTAGTGATGCAAAACTAACGGGTTAAGAAATAAAAAGGTTGGT 576793
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                                  8730 ATCAGCATIGAIGCACTITIAGAAGCGGTTGGGAIGGAIAGTTGCAAAAAGAAGCTICCT 78789
                                                                                                                                              78790 AATGAATTGAGTGGTGGCGAACAGCAACGTGTTTCCATTGCAAGAGCTTTTGCTAAAAAC 78849
                                                                                                                                                                                                                                          78850 CCCTTATTAATTTTTGGTGATGAACCTACTAGGGCACTTGATCTTGAGATGACCCAAATT 78909
                                                                                                                                                                                             127 TIGCICAACIGICTIGGCACACTIGACAAACCAAGITCCGGACAGAICCTIGICGAGGAT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGGTGGAAAAACACAAATGGCCTGAAATTCCTC----AAGTACTTCATGCTGTTGGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 CITGAGTCGTTCGAGGAAAAGCCAGTTTTGAACTCTCTGGTGGCGAACACAACAACAACT 420
328 CCTGAAATTCCTCAAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 AAGTITITACCAGGAACAATGACAGCACTGACTGGAGCGTCCGGTTCAGGAAAATCGACT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 GTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAAAATACGGTGGGC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 TATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAATTCAACCTTCAGCTT 306
                                                                                              388 TITGAACTCTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/545,528D CURRENT FILING DATE: 1995-10-19 PRIOR APPLICATION NUMBER: US 08/488,018 PRIOR PLICATION NUMBER: US 08/483,545 PRIOR APPLICATION NUMBER: US 08/473,545 PRIOR FILING DATE: 1995-06-07
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                                                                                                                                                                                                                                                                                            508 GTCATAGAAGCATTGAGAGCACT 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
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Best Local Similarity 50.19
Matches 216; Conservative
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                                            .5021 TGATGAAGGGGAAATCTGGATTGATGGTGTTAATATTGGGGATTATAGTTCCCACCAGGG 15080
                                                                                                                                           15081 CACCAATTACCGTAGAAATGATGTGGGGTTTGTTTTTTATAATCTAGTTTCTAA 15140
                                                                                                                                                                                                                                             15141 TCTGACAGCTAAGGAAAATGTGGAACTGGCTTCTGAAATTGTGACAGATGCCTTGAATCC 15200
                                                                                                                                                                                                                                                                                                                                         15201 TGATCAGGCCTTGACAGATGTAGGTCTGGCTCATCGTCTCAATAACTTTCCAGCCCAGCT 15260
                                                                                                                                                                                                                                                                                                                                                                                                                                        15261 TTCTGGAGGGAGCAACAGCGAGTCTCCATTGCACGCGGGTAGCCAAAAATCCTAAAAT 15320
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                                                                                                                                                                                             279 CAGGACAGTIAAATICAACCTICAGCTIGGGGIGGAAAAACACAAATGGCCTGAAATICC 338
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159 AAGTICCGGACAGAICCTIGICGAGGAIGIAGACCTICIGAAACICICIATACGCGIAAAGCA 218
                                                                                                                                                                                                                                                                                            339 ---TCAAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACT 395
                                                                                                                                                                                                                                                                                                                                                                                           CTCTGGTGGCGAACAACGAACGGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCGGAAT 455
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                                                                                              219 ACGGITATACAGGAAAATACGGIGGGCTATTITATTICAAGATTATGCCTIGATICCCGA
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Best Local Similarity 50.1%; Pred. No. 2.6e-14;
Matches 222; Conservative 0; Mismatches 209; Indels 12; Gaps
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Patent No. 6537773
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CRGANISM: Mycoplasma genitalium
US-08-545-528D-1
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LENGTH: 580073
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Sequence 1259, Application US/09543681A
Patent No. 6605709
Patent No. 6605709
Patent No. 6605709
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT PILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
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                                                                                                                 TCCTCAAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACT
                                                                                                                                                           468 TGTAGAGGTATTGAGGCAAGTGGGCCTAGCTCATCGATTGAATAACTTTCCGTCCCAATT
                                                                                                                                                                                                    396 CTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAATCCCCGGAAT
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Pred. No. 5.8e-15;
0; Mismatches 239;
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Best Local Similarity 47.4%;
Matches 215; Conservative
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                                                                                                                                                                                                              APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 AAGTICCGGACAGATCCTTGICGAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCA 218
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11.8%; Score 71.8; DB 4; Length 8
Best Local Similarity 49.6%; Pred. No. 4.1e-15;
Matches 212; Conservative 0; Mismatches 212; Indels
                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
NAME/KEY: misc_feature
;
LOCATION: (B) LOCATION 1...813
;
SEQUENCE DESCRIPTION: SEQ ID NO: 3565:
US-09-107-532A-3565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Enterococcus faecium
                                                                                                                                           Sequence 3565, Application US/09107532A
Patent No. 688275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3565:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 813 base pairs
                                                                                                                                                                                                                                                                                                                                                                    CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                     576552 dcagirakrar 576542
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM
GCTCTAGATTT 491
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
ORIGINAL SOURCE:
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481
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g ò 셤 ò q 'n 136

Gaps

154

256 274 311

214

358 394 418 454 478 514 538

334

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137 GTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTCGAGGATGTAGACCTTC 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 AGAATTTTAGTTTAATTGAAACACTAACAGTTGAAGAAACATTGAATTACCTCTTTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 ATAGTGGGTTÄÄCCCCÄÄÄAGAAGCCÄÄÄGATCGTGTCCACGÄÄGTTCTGACAAAÄTCG
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Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Score 69.6; DB 4; 1
Pred. No. 2.2e-14;
0; Mismatches 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          539 AAGGCGCCACGTTGTTGTTGCTACGCA 566
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FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                           ; ORGANISM: Enterococcus faecalis US-09-134-000C-2474
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 49.4%;
Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Maryland COUNTRY: USA
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US-08-956-171E-96
                                                                                                                                                                                                                                SEQ ID NO 2474
LENGTH: 681
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                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM:
                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                        GENERAL INCORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
DOUGETE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: S674
SEQ ID NO 1763
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Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
APPLICANTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --AAGTACTICAIGCIGIIGGICIIGAGICGIICGAGGAAAAGCCAGIITIIGAACICIC 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 aditgaadgeaaagaaathaaraaaddgagecacaaaagaagtgegaaatittegaaaada 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---- 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTCGAGGATGTAGACCTTCTGAAACTCTTACGCGTAAGCAACGGTTATACAGGAAAAA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 TACGGTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAATTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 ICICAGICAIAAGTITITACCAGGAACAAIGACAGCACTGACTGGAGCGTCCGGTTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATAAGTTTTTCAGTTGAAAAGGGGAATTTGTAGCTGTCATGGGTCCTTCTGGATCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 71.2; DB 4; Length 771;
Pred. No. 6.5e-15;
0; Mismatches 213; Indels 18
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                                                                                     GATGAACCAACCGGAGCTCTAGATTTAACAAACA
                                                                                                                                                                                                                                                          Sequence 1763, Application US/09134001C
Patent No. 6380370
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US-09-134-001C-1763
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Best Local Similarity 49.6
Matches 227; Conservative
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US-09-134-000C-2474
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Gary Breton et. al
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Best Local Similarity 46.0
Matches 225, Conservative
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                                MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
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Pred. No. 3.4e-13;
                                                               OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                 PRICR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 3, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY AGRET INFORMATION:
NAME: Mark J. Hyman
REFERENCE/DOCKET NUMBER: 46,789
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear seq ID NO: US-08-956-171E-96
                                                                                                                                                                                                                                                                                                                                           301) 309-8439 (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 11050 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                  COMPUTER READABLE FORM
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Matches 226; Conservative
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US-09-489-039A-3320
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Sequence 3320, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERSENCE: 2709,2004001
CURRENT APPLICATION NUMBER: 105/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 3320
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Sequence 2762, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Dowcette-Stamm et al
APPLICANT: Lynn Dowcette-Stamm et al
APPLICANT: Lynn Dowcette-Stamm et al
APPLICANT: Lynn Dowcette-Stamm et al
APPLICANT: Lynn Dowcette-Stamm et al
APPLICANT: Lynn Dowcette-Stamm et al
APPLICANTON: WINTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 032796-032
CURRENT APPLICATION NUMBER: US 60/055,778
FRIOR APPLICATION NUMBER: US 60/055,778
FRIOR APPLICATION NUMBER: US 60/055,778
FRIOR PRING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SCOFTWARE: Patentin version 3.1
SEQ ID NO 2762
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Pred. No. 3.7e-13;
0; Mismatches 264;
                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Klebsiella pneumoniae
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207 GCCATCATGGGTGAGTCTGGTTCTGGTAAATCAACTCTTCTCAATATTTCTAGCTATGTTG 266
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 72, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
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                                                                                                                       341 AAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTG 400
                                                                                                                                                                                GTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCGGAATAATTC 460
                                                                                                                                                                                                                                                                           533 TGGCTGATGAACCGACTGGGGCCATTGGATAGTGAAAACGGGTACAGAAATTATGGAATTAT 592
                                                                                                                                                   <u> Aatracctraaaartigicegtrigeaaacaaaaeceaaatcaaaagtracteaactricte</u>
                                                                                                                                                                                                             TGGCTGATGAACCAACCGGAGCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCAT
                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                          TGAGAGCACTCGCCGACAAAGGCGCCACCGTTGTTGTTGCTACGCA 566
                                                                                                                                                                                                                                                                                                                                     reaaagaarrgaacaggggaaaggarrgrcargargacaca 638
                                                           Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 4; Length 148
Pred. No. 6.7e-12;
0; Mismatches 235; Indels
                                                           Score 66; DB 4; Length 720
Pred. No. 4.4e-13;
0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.50 inch, 1. COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text SOFTWARE: ASCII Text APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brookes, A. Anders
REGITRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB34(
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 49.1%;
Matches 244; Conservative 0
                                                           10.8%;
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nucleic acid
EDNESS: double
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                                                          Query Match
Best Local Similarity 55.8
Matches 126; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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COMPUTER READABLE FORM:
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US-08-961-527-72
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91 GCACTGACTGGAGCGTCCGGTTCAGGAAAATCGACTTTGGTCAACTGTTTGGCACACTT 150

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US-09-134-001C-1758
US-09-134-001C-1758
Sequence 1758, Application US/09134001C
Patent No. (6380370)
GENERAL INFORMATION:
TITLE DE INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE DE INVENTION: DEPLERANDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE DE INVENTION: DEPLEMENTION SPACE OF TITLE REFERENCE: GTC-007
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR FILING DATE: 1997-11-06
PRIOR FILING DATE: 1997-11-06
PRIOR FILING DATE: 1997-10-14
SEQ ID NO 1758
LENGTH: 11-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     567 GCCATCATCACAAACTTGTGTTGTGGGACGAGGCGAGGGGGGGCCTTGATTCC 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAAACAGIGAGCIAGICAIAGAAGCAITGAGAGCACICGCCGACAAAGGCGCCACCGIT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGTCATCTGCAGCCTTACTTGATGTCTTTAATGAATCAATGAGCGTGGGCAAACCATC 686
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GACAAACCAAGTTCCGGACAGATCCTTGTCGAGGATGTAGACCTTCTGAAACTCTTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                  447 ATAACGGAGATGATGAAGAAATTGGTGGTGACAGCTGAGAATCTGGGTATTAACCAATTG
                                                           267 GATAAACCAAGTCGTGGTCAGGTTTACTTGAATGGAACTGACACCGCAACTATTAAAAAT
                                                                                                                                                                                                                                     271 ATTCCCGACAGGACAGTTAAATTCAACCTTCAGCTTGCGGTGGAAAAACACAAATGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACAACTGCGTTGGCCCGG
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                                                                                                                    83 TITITGAAAGACATAGATATICATATIGAIGAAGGIGAATITATIGCIATCAIGGGICCGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        553 GITGITGCIACGCACIC 569
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Best Local Similarity 47.23
Matches 250; Conservative
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494 GGGCAATTGTTAATGAGCCTGAAATÁTTATTAGATGAGTCTTTATCCGCATTAGATT 553
374 GTAAGTCAGAAATTAAGCGTAAGGTTACTGAAGCACTTCAGTTGGTGAAATTAAGTGGTT 433
                                                                                                          434 ATGAACATAGGCAAATACAAGGTATGAGTGGTGGACAAAAACAACGTGTAGCCATAGCAC
                                                        MCS-09-121-017B-187/c
; Sequence 187, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
APPLICANT: Ross, Bruce C.
ITLE OF INVENTION:
P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
CONRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CONTRY: CA
CONNTRY: USA
                                                                                                                                                                                                                                                                             491 TAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACT 530
                                                                                                                                                                                                                                                                                                                               554 rahahregaacegaangcaheretraridakkaker 593
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FastSEQ for Windows Version 2.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUSENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT/AU98/01023
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REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2734(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEPAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCTAU98
FILING DATE: IN-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P91182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION NUMBER: PP1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COINTRIE CONTURE I CONTURE I COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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INPORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 4635 base pairs
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Patent No. 6380370

Patent No. 6380370

ABRIEGATI INFORMATION:

APPLICANT: LYMN DOUGETE-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: BFIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: US/09/134,001C

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US/09/134,001C

PRIOR FILING DATE: 1997-01-08

PRIOR FILING DATE: 1997-01-08

PRIOR FILING DATE: 1997-01-08-14

NUMBER: OF SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATITICAAGATTATGCCTTGATTCCCGACAGGACAGTTAAATTCAACCTTCAGCTTGCGG 310
                                                                                                                   ---AAAAACACAAATGGC 328
                                                                                                                                                                                                                              329 CTGAAATTCCTCAAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTT 388
                                                                                                                                                                                                                                                                          383 GCAAAGTITTAGACGACTTCATGACGTCGGTCTAAAAGGTAAAAGGAATCTCTTACCAA 442
                                                                                                                                                                                                                                                                                                                                                                                              443 ATAAATTGTCAGGAGGGCAGCAACAACGTGTAGCTATTGCCCGGGCAATTATTAATGACC 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                   503 CTAAGITTATTATTGCCGATGAACCTACTGGCGCTCTTGATTCGAAGACATCTCAAGATA 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 ingaaccaccoranninaracachanaderecencaccinorecaaaaacaacaanin 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 TAPAACTCATAGCAGGATTTGAATATCCCGATAGTGGAGATATTATATAAAGATAAAC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 ACCTICTGAAACTCTTACGCGTAAGCAACGGTTATACAGGAAAAATACGGTGGGCTATT 250
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     227 ACAGGAAAATACGGTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAG 286
                                                           263 Trccaaarcaracreracerrescriricagaarrraaarreararaaaraaacacra 322
                                                                                                                                                                     323 Trttagaaaargratrcccchaartrataargctrigagraaaaaaaa 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509 TCATAGAAGCATTGAGAGCACTCGCCGACAAAGGCGCCACCGTTGTTGTT 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 TTATGGAGCTTTTCGTAAACTGAACAAAACAGAACAGATACAACTATTATT 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.5%; Score 64; DB 4; Length 1149; Best Local Similarity 45.2%; Pred. No. 3e-12; Matches 235; Conservative 0; Mismatches 285; Indels
                                                                                                                   287 TIAAATICAACCIICAGCIIGGGGIGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-134-001C-602
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LENGTH: 1149
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3466760 TCCCCGAAGTGCTCGAGACGGTCGGTCTGTCCGGCAAGCCAATCGGCTGCCAGACGAGC 3466701
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                                                                                                                                                                     1674 TCAGCTCTCCGCAGGACAACAGCAGCGCGTGCTATCGCCCGTGCCGTGGTGGCCAATCC 1615
                                                                                                                                                                                                                        509
                                                                                                                                  449
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                                                                                                                                                                                                                                                                                                                                                   1554 CATGGAACTGCTCAGAGGTCTCAATCGCGAAGGTGCAACCATCGTCATGGTGACGCACTC 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 TTCCTCAAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAAC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCGGAA 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: CDC 1551
CHER INFORMATION: "n" bases at various positions throughout the sequence J OTHER INFORMATION: represent a, t, c or g
                                                                                                                               390 TGAACTCTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCCGGGTACTGCTCAAAAATCC
                                                                                                                                                                                                                   1614 GAAGCTCATCCTCGCCGATGAACCCACGGTAACCTCGACTCAAAAACGGAGCCGATGT
                                                                                                                                                                                                                                                                                                         510 CATAGAAGCATTGAGAGCACTCGCCGACAAAGGCGCCACCGTTGTTGCTACTACGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      515 AAGCATTGAGAGCACTCGCCGACAAAGGCGCCACCGTTGTTGTTGCTACGCACTCGCCCC
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
                                                                                        .;
0
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                                            Length 4635;
                                                                                      97; Indels
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Pred. No. 1.7e-09;
0; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         1494 CGAGCACGATGCACGTAGTCCCCCCCCATCATCT 1456
                                                                                                                                                                                                                                                                                                                                                                                               570 GCCCCTCTTCCGAGAATCAGCGGATACCATTATCAAACT
                                         Score 63.8; DB 4;
Pred. No. 8.5e-12;
0; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09103840A Patent No. 629428 GENERAL INFORMATION APPLICANT: FLEISCHMAN, ROBERT D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3466520 ACATCGTCGACTC 3466508
                                         Query Match
Best Local Similarity 55.7%;
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.3%;
Best Local Similarity 53.0%;
Matches 134; Conservative
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US-09-103-840A-2/c
US-09-221-017B-187
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Search completed: July 30, 2004, 14:16:21 Job time: 111 secs
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

T/40. Finding

- nucleic search, using sw model OM nucleic

July 30, 2004, 13:27:50 ; Search time 506 Seconds (without alignments) 5901.210 Million cell updates/sec Run on:

US-09-868-338-7_COPY_1117_1725 Title: Perfect score: Sequence:

1 atgatagaaatcaatgacct.........cggataccattatcaaacta 609

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3222919 seqs, 2451570024 residues Searched:

6445838 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT7_MBW PUB.seq:*
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17: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Seminary of April	Segment 2058 An	Sequence 9384 An	Segmence 36, April	Sequence 3886. An	Segmence 27244. A	Semience 13 April	Semience 13. April		Segmente 1 Appli	Segment L April	Segmence 34668 b	Segment 3820 An	Sequence 30817, A
ΙD	16 US-10-398-221-9	16 US-10-398-221-2058	US-09-815-242-9384	US-10-158-844-36	US-10-398-221-3886	US-10-282-122A-27244	US-09-960-870-13	US-09-960-858-13	US-10-251-668-13	US-10-205-220-1	US-10-205-220-1	US-10-282-122A-34668	US-10-398-221-3820	US-10-282-122A-30817
DB	16		σ	13	16	13	10	10	13	15	15	13	16	13
% Query Match Length DB	684707	3011208	711	21706		1401		31241		Ñ	580073		5312	
% Query Match	13,3	13.3	12.7	12.4	12.3	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.1	12.0
Score	80.8	80.8	77.4	75.4	75	74.6	74.6	74.6	74.6	74.6	74.6	74.4	73.6	73.2
Result No.		ر 2	m	4	บ	9	7	80	σ	10	c 11	12	13	14

Semience 956. App	441	equence 1	equence 329	equence 7.	123,	equence 12,	equence 3.	96	e 96.	6038	238,	101	27		37	72	quence 68.	18.	17	equence 6.	20	e 10	252	equence 9592	e 3588. A	239	2421,	ce 195,	e 29,	ന
US-09-738-626-956	3 US-10-627-476-441	US-09-738-626-1		US-10-398-2	US-09-070-927A-123	US-10-307-29	US-10-307-294-	08-781-986A-9	S	-815-242-603	-09-070-927A-	US-10-282-122A-10	US-10-282-122A-27	US-10-282-122A-24	US-10-398-221-37	US-10-158-844-7	-070-927A-6	US-10-19	US-10-398-221-1	US-10-398-221-	6 US-10-398-221-2	6 US-10-398-221-1	-09-815-242-925	09-815-242-959	₽	US-10-282-122A-23	242	US-10-158-844-1	US-10-114-17	US-09-769-787-3
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11.9	11.9		•	11.7	11.4	11.3	11.3	11.2	11.2	11.2	10.8	10.8	10.7	10.7	10.7	٥.	0	10.5	ö	10.3	ö	ö	ö	10.2	10.2	10.1	10.1	10.0	10.0	10.0
72.4	N	72.4	71.6	н	9.69	œ	œ	68.4	œ.		Q	65,6	'n	65	65	φ	4.	•	ë.	63	9	'n	•	'n	62	61.6	•	61		60.8
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ALIGNMENTS

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346005 AIGATIGAATIAGITAATGICAGIAAAAGATACAAGATAAATIGATITIGGAAAAAGIC 346064
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Best Local Similarity 47.2%; Pred. No. 5.3e-14;
Matches 284; Conservative 0; Mismatches 312; Indels 6;
US-10-398-221-9

Sequence 9, Application US/10398221

Fublication No. US20040018514A1

Fublication No. US20040018514A1

APPLICANT: KUNST, Frederik

APPLICANT: GLASER, Philippe

TITLE OF INVENTION: Listeria innocua, genome and applications

FILE REFERENCE: 344 702 - US

CURRENT PRILIG DATE: 2003-03-27

FRIOR APPLICATION NUMBER: DCT/FR 01/03 061

FRIOR APPLICATION NUMBER: FR 00/12 697

FRIOR PILING DATE: 2001-10-04

FRIOR PILING DATE: 2001-10-04

FRIOR PILING DATE: 2001-10-04

FRIOR PILING DATE: 2001-10-04

FRIOR PILING DATE: 2001-10-04

FRIOR PILING DATE: 2001-10-04

FRIOR PILING DATE: 2001-10-04

FRIOR FILING DATE: 2001-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature; LOCATION: (1)...(end)
) LOCATION: (1)...(end)
US-10-398-221-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Listeria innocua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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121 TCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTC 180
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT TILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2001-22-22
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Patent No. US202006156951
GENERAL INFORMATION:
APPLICANT: Hasalbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2934749 referireratigaagergeceaarriatricagiceredeceagagigeragigeaag 2934690
                                                                                                                                                                                                                                                                                        346239 TTAGGTTTTATATTCCAAAATTATCTATTGGAAAATGAAAGGGTGTTAGAAAACTTA 346298
                                                                                                                                                                                                         346185 AACGAGATGGAATATCAGA-----CGAAAAAAGAGGTTATGACTCTAAAAAAAAGAGGTG 346238
                                                                                                                                                                                                                                                                                                                                                                                                                  346299 TCCATTACAGGTGGGGAAAATCGCAAGCTGATGATAGAGCATTTGGAAGAAGTAGGAATG 346358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346359 GATGAGAGCTATTTAGCAAAAAAGTATACCAATTAAGTGGTGGAGAAAAACAACGGATT 346418
346065 TCTCTTTCTATTGGAGCTGGCGAATTTATTGCAGTCGGCGAGAGTGGTAGTGGGAAG 346124
                                                                                                   346125 ACAACGCTGCTAAATGTTATCGGACACCTAGATTCAAAAGATAGTGGGCAAGTTAŤTAŤT 346184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346419 GCTATTGTGCGCATTTTACTCAAACCATTTCAACTTTTACTTGCGGACGAACCAACTGGC 346478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346479 AATTTÄGATGATAAAAACAAAAAATCATTGAATTATTTCTAGCCTTGAAAAAGCAA 346538
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                                                                                                                                                                                                                                                                                                                                                                  301 CAGCTTGCGGTGGAAAAACACAAATGGCCTGAAATTCCTCAAGTACTTCATGCTGTTTGGT 360
                                                                                                                                                         181 GAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAAAATACG 240
                                                                                                                                                                                                                                                         361 CTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACAACT 420
                                                121 TCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 GOGGCCACCGTTGTTGCTACGCACTCGCCCCTCTTCCGAGAATCAGCGGATACCATT 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 GCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGACAAA
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US-10-399-221-2058/C
Sequence 2058, Application US/10398221
Sequence 2058, Application US/10398221
Sequence 2058, Application US/10398221
Sequence 2058, Application US/10398221
Setural INFORMATION:
FAPLICANT: GLASER, Palilippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REPERRANCE: 344 702 - US/10/398,221
CURRENT FILING DATE: 2003-03-27
FRIOR PELING DATE: 2003-03-27
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: PatentIn version 3.0
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13.3%; Score 80.8; DB 16; Length 3
Best Local Similarity 47.2%; Pred. No. 1.2e-13;
Matches 284; Conservative 0; Mismatches 312; Indels
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US-10-398-221-2058
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2934689 ACAACGCTGCTAAATGTTATCGCACACCTAGATTCAAAAGATAGTGGGCAAGTTATT 2934630
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                                                                                         181 GAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAAATACG 240
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APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REPERBNCE: 34 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT PILING DATE: 2003-03-27
PRIOR PLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
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                                                                                                                                                                                                                                                                                                                            Score 75.4; DB 13;
Pred. No. 4.5e-13;
0; Mismatches 206;
FILING DATE: 1996-10-31
ATTOREY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
ERFERENCE/DOCKET NUMBER: PB340P1D1
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 36: US-10-158-844-36
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; Sequence 386, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
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ORGANISM: Listeria monocytogenes 4b
FEATURE:
                                                                                                                                                                 LENGTH: 21706 base pairs
                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                 12.4%;
50.4%;
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SEQ ID NO 3886
LENGTH: 12278
                                                                                                                                                                                                                                                                                                                                                                              212; Conservative
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Best Local Similarity
Matches 212; Conserv
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Sequence 36, Application US/10158844
Publication No. US20040029118A1
GENERAL INFORMATION:
APPLICANT: Kunsch et al.
TITLE OF INFORMINES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                   82 GATGTGAATTTTGAGATTGAAAAGGGGGAACTGGTTATTATCCTTGGTGCTTCAGGTGCA 141
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                                                                                                                                                                                        Length 711;
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                                                                                                                                                                                     Score 77.4; DB 9; Length 7
Pred. No. 1.4e-14;
0; Mismatches 226; Indels
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/961,527
PILING DATE: 1997-10-30
APPLICATION NUMBER: US 60/029,960
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APPLICATION NUMBER: US/10/158,844
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OPERATING SYSTEM: Windows
SOFTWARE: ASCII Text
                        TYPE: DNA ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                        12.7%;
50.8%;
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COMPUTER READABLE FORM:
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                                                                                                                                                                                     Query Match
Best Local Similarity 50.8
Matches 236; Conservative
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                                                                                                                     .. (711)
                                                                                         NAME/KEY: CDS

LOCATION: (1)...

US-09-815-242-9384
  LENGTH: 711
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CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
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US-09-960-870-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9196 TCCATTACAGGTGGGAAAATCGCAAGCTGATGATAGAGCATTTAGAAGAAGTAGGAATG 9137
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                    1 ATGATAGAAATCAATGACCTCAAGAAATCTTTTGGCGTTCGGATCTTATGGCAAGGTCTC
                                                                                                                                             9
                                                                                                           Length 12278;
                                                                                                       Score 75; DB 16; Length 12
Pred. No. 4.4e-13;
0; Mismatches 316; Indels
; NAME/KEY: misc_feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
US-10-398-221-3886
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Reri
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Trawick, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Paramoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
                                                                                                       12.3%;
ilarity 46.5%;
Conservative C
                                                                                                                       Similarity
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SOFTWARE: Patentin version 3.1
SEQ ID NO 27244
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Pred. No. 1.7e-13;
0; Mismatches 209; Indels
PRIOR APPLICATION NUMBER: 60/20, 9 PRIOR FILING DATE: 2000-03-21 PRIOR PILING DATE: 2000-03-21 PRIOR FILING DATE: 2000-03-21 PRIOR FILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: 60/20, 335 PRIOR FILING DATE: 2000-05-06 PRIOR FILING DATE: 2000-09-09 PRIOR FILING DATE: 2000-09-09 PRIOR FILING DATE: 2000-09-09 PRIOR PILING DATE: 2000-10-23 PRIOR APPLICATION NUMBER: 60/23, 625 PRIOR APPLICATION NUMBER: 60/23, 625 PRIOR PELING DATE: 2000-11-27 PRIOR PELING DATE: 2000-11-27 PRIOR PELING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-12-22 PRIOR FILING DATE: 2000-12-22 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-16
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US-10-282-122A-27244
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ilarity 50.1%;
Conservative
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Best Local Similarity
Matches 222; Conserv
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                                                                       8214 edecerricadaricredrahahacefahahacariarirreaggarigariadager 8273
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Sequence 13, Application US/10251668

Publication No. US20040063097A1

GENERAL INFORMATION:
APPLICANT: Brans, Glen
TITLE OF INVENTION: USE
TITLE OF INVENTION: USE
TITLE OF INVENTION: USE
CURRENT APPLICATION NUMBER: US/10/251,668

CURRENT FILING DATE: 2002-09-20

PRIOR PILING DATE: 2001-09-20

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 31241
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12.2%; Score 74.6; DB 13; Length Best Local Similarity 50.1%; Pred. No. 1e-12;
Matches 222; Conservative 0; Mismatches 209; Indels
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, ORGANISM: M. genitalium
US-10-251-668-13
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US-10-251-668-13
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                                                                                                                                                                                                                                                                                                                                                                         Score 74.6; DB 10; Length 3:
Pred. No. 1e-12;
0; Mismatches 209; Indels
APPLICANT: Evans, Glen
TITLE OF INVENTION: NANOMACHINE COMPOSITIONS AND METHODS OF
TITLE OF INVENTION: NANOMACHINE COMPOSITIONS AND METHODS OF
TITLE OF INVENTION OF 108
CURRENT APPLICATION NUMBER: US/09/960,870
CURRENT FILING DATE: 2001-09-20
NUMBER OF SEQ ID MOS: 19
SOFTMARE: FASELSEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.2%; Score 74.6; DB 10; Length ilarity 50.1%; Pred. No. 1e-12; Conservative 0; Mismatches 209; Indels
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                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.1%;
Matches 222; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: M. genitalium
US-09-960-858-13
                                                                                                                                                                                                                                                                       ; TYPE: DNA; CRGANISM: M. genitalium
US-09-960-870-13
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Best Local Simil
Matches 222; C
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LENGTH: 31241
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US-09-960-858-13
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APPLICANT: Fraser et al.

TITLE OF INVENTION: Unclectide Sequence of the Mycoplasma Genitalium Genome, Fragments TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB193P1D1
CURRENT APPLICATION NUMBER: US/10/205,220
CURRENT APPLICATION NUMBER: US/08/45,528
RICH APPLICATION NUMBER: US 08/445,528
PRICH APPLICATION NUMBER: US 08/488,018
PRICH APPLICATION NUMBER: US 08/488,018
PRICH APPLICATION NUMBER: US 08/473,545
PRICH APPLICATION NUMBER: US 08/473,545
NUMBER OF SEO ID NOS: 1
SOFTWARE: PatentIn version 3.1
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Pred. No. 5.4e-12;
0; Mismatches 209;
                                                                                                                78910 Girriaaaacagirrraacaar 78932
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US-10-282-122A-34668
; Sequence 34668, Application US/10282122A
                                                                       GTCATAGAAGCATTGAGAGCACT 530
                                                                                                                                                                                                                        Sequence 1, Application US/10205220 Publication No. US20030170663A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
US-10-205-220-1
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Best Local Similarity 50.1%;
Matches 216; Conservative C
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US-10-205-220-1/c
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TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
FILE REPERBNCE: PB193P101
CURRENT APPLICATION NUMBER: US/10/205,220
PRIOR APPLICATION NUMBER: US 08/545,528
PRIOR FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/473,545
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 1
SCOFTMARE: Patentin version 3.1

LENGTH: 580073
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  3394 ITAACAGTTAGAGAAAACAITGAGATAGGAGCAAATCTTCAACCAGATCCTAGTAAAAGG 8453
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                                                                                                                                388 ITTGAACTCTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGGTACTGCTCAAAAT
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Publication No. US20030170663A1
GENERAL INFORMATION:
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; ORGANISM: Mycoplasma genitalium
US-10-205-220-1
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                                               TGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGGTACTGCTCAAAAATCCCCGAATAAT 458
432 rescesarchechachacsacscesecesecesecentes de 1911 a 1911
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| Publication No. US20040018514A1
| GENERAL INFORMATION:
| APPLICANT: KUNST, Frederik
| APPLICANT: KUNST, Frederik
| APPLICANT: GLASER, Philippe
| TILE OF INVENTION: Listeria innocua, genome and applications
| FILE REFERENCE: 344 702 - US
| CURRENT FILING LISTER: 2001-00-04
| CURRENT FILING DATE: 2001-10-04
| PRIOR FILING DATE: 2001-10-04
| PRIOR FILING DATE: 2001-10-04
| NUMBER OF SEQ ID NOS: 4025
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 3820
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; OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
US-10-398-221-3820
                                                                                                                                      459 TCTGGCTGATGAACCAACCGGAGCTCTAGATTTAACAA 496
                                                                                                                                                                               492 irricecagarcaaccraciedececarragaricraaaa 529
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Pred. No. 7.9e-13;
0; Mismatches 229;
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ORGANISM: Listeria monocytogenes 4b
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50.2%;
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Best Local Similarity 50.2
Matches 234; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 TAAAACGACTTTACTCAATGTGTTAAGTTCAATAGATACTATTTCAGGAGGAACTGTAGA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 TGTCGAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAAAA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTIGAAGGIAAAGAAAÍTAATAAACIGAGCCACAAAAGAAGIGGCAAATTITICGAAAACA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 ACATCTCGGTTTTATTTTCAAGATTATAGCGTTTTACCCACATTAACAGTAAAAGAAAA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 TATTATGCTACCACTCTCAGTACAAAATTCCATAAATATGAAATGGAACAAATTATAA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --AAGTACTICATGCTGGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CANT: Xu, H. OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                 NERNT FILING DATE: 2003-02-20
OR APPLICATION NUMBER: 60/191,078
OR FILING DATE: 2000-03-21
OR APPLICATION NUMBER: 60/206,848
OR FILING DATE: 2000-05-23
OR APPLICATION NUMBER: 60/207,727
OR APPLICATION NUMBER: 60/207,727
OR APPLICATION NUMBER: 60/207,335
OR APPLICATION NUMBER: 60/203,347
OR APPLICATION NUMBER: 60/230,347
OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-09-09
OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-12-3
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/267,931
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
Remaining Date: 2001-02-16
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US-10-282-122A-34668
                                               Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
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50.0%;
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local
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Application US/09738626
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Publication No.
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; ORGANISM: Cor
US-09-738-626-956
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APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Grant
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APPLICANT: Foreyth, R.
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APPLICANT: Eoreyth, R.
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APPLICANT: Eoreyth, R.
APPLICANT: Sull Resemble R. Us/10/282,122A
TILE REFERENCE: BLITRA. 034A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-06
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-10-33
PRIOR FILING DATE: 2000-10-36
PRIOR FILING DATE: 2000-11-27
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PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-10-23
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PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-24
PRIOR PLING DATE: 2000-10-20-6
PRIOR PLING DATE: 2000-10-20-6
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 richinghahcachachninanhchahaganncocncanghchcechcninghagacanch
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12.0%; Score 73.2; DB 13; Length 684;
Best Local Similarity 46.4%; Pred. No. 3.3e-13;
Matches 283; Conservative 0; Mismatches 318; Indels 9
                                   Sequence 30817, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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; ORGANISM: Pasteurella multocida
US-10-282-122A-30817
                                                                                                                                                                                                                                   Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
                                                                                                                                 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
       .10-282-122A-30817
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242 TCGGTCTGGTCTTTCAGCAATTCCACTTAATCCCTTTTTAACTGCCTTGGAAAACGTCA 301
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11.9%; Score 72.4; DB 9; Length 6
Best Local Similarity 47.4%; Pred. No. 6e-13;
Matches 257; Conservative 0; Mismatches 276; Indels
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APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVARINON: NOVEL POLYNUCLEOTIDES
TITLE OF INVARINON: 1299-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-16
PRIOR PLLING DATE: 2000-08-03
NUMBER OF SEC ID NOS: 7059
SOFTWARE: PALENTIN VOET: 3.0
SEC ID NO 956
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SEC IN NOS: 7059
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                                 226 TCAGACCTCAACGCCAAACGCGAGCTGAAACCAGGCGTCGCCACATCGGAGTTATTTTC 285
                                                                     256 CAAGATTATGCCTTGATTCCCGACAGACAGTTAAATTCAACCTTCAGCTTGCGGTGGAA 315
                                                                                               316 ------AAACACAAATGGCCTGAAATTCCTCAAGTACTTCATGCTGTTGGTCTTGAG 366
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Schistosoma mansoni

Schistosoma mansoni

Bukaryota; Metaaca; Platyhelminthes; Trematoda; Digenea;

Bukaryota; Metaaca; Platyhelminthes; Trematoda; Digenea;

Striggidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

Striggidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

Striggidida; Schistosomatoidea; Martins, E.A.L., Guimaraes, P.E.M., Orlopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr., Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F., Colson, P.S., Dillon, C.P., Pariss, L.P., Gregorio, S.P., Ho, P.L., Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A., Nascimento, A.L.T.O., Ohlweller, F.P., Reis, E.M., Ribeiro, M.A., Say, R.G., Stukart, G.C., Scares, M. B., Gargioni, C., Kawano, T., Schubal, J.C., Laite, L.C.C. and Dias-Neto, E.

Transcriptome analysis of the accelomate human parasite Schistosoma
CD740366 4029716 1
CD731492 40405911
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ML1-0091T-L258-D10-U.B ML1-0091 Schistosoma mansoni cDNA clone
ML1-0091T-L258-D10.B, mRNA sequence.
CD164788.1 GI:34701451
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DEFINITION
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VERSION
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AUTHORS
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Score

Result No.

Post-processing:

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Minimum DB seq Maximum DB seq

Scoring table:

Searched:

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/note="Vector: pcosRW2; Site 1: SpeI; Pulsed-field gel purified DNA from Western X-disease phytoplasma was digested to completion with SpeI and cloned into the AvrII site of pcosRW2. PoosRW2 was first modified by inscrting an annealed oligonucleotide containing the recognition sequences for AvrII, NcoI and MluI into the EcoRI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CG954936 639 bp DNA linear GSS 15-DEC-2003
MBEBP10TF mth2 Medicago truncatula genomic clone 20B20, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 GGAGCGICCGGTTCAGGAAAATCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 TITGAACTCTCTGTGGGGGAACAACAACGAACTGGGTTGGCCGGGGTACTGCTCAAAAAT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    456 AACGAATTATCAGGCGGACAAAAACAAAGAATAGCCATCGCTCGTGCTTTGGTTAAAAT 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sie ecggagaitaititageggatgaaceaacaacerggaiteaaaactgggassassa 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 ggaaaarcaggarcagacaaarcgacrcrrraaacrcgriggaggacaacrcgaraagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 gatagrigagaratartaratrakaritrorrakararakartararakarakarakaraka 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 gacgacratriaakogcgratriaggcrirraritriccaagaarirraariraaraagaagr 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 angaangrinangaaaanancecrinagcraangagcrincaggecraaaaaccggacaar 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 CCTGAAATTCCTCAAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 AAACTAATTTATAACTTATTAAAAGAAATGGAACTTTTAGGTTATGAAGAAAAAATT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGACAGTTAAATTCAACCT-----TCAGCTTGCGGTGGAAAACACAAATGG 327
One Shields Ave, Davis, CA 95616, USA
Tel: 530 752 1697
Exa: 530 752 5674
Email: cwling@ucdavis.edu
Sequences were manually edited using Sequencher to remove vector and low quality sequence.
Seq primer: SP6
Seq primer: SP6
Class: cosmid ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 AGTICCGGACAGATCCTTGTCGAGGATGTAGACCTTCTGAAACTCTTACGCGTAAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 CGGTTATACAGGAAAATACGGTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Western X-disease phytoplasma SpeI cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.4%; Score 63.4; DB 28; Length (48.5%; Pred. No. 1.4e-08; ative 0; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                            organism="Western X phytoplasma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="Jensen"
/db_xref="taxon:37704"
/clone="$2H2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  508 GTCATAGAAGCATTGAGAGGACT 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG954936.1 GI:39870005
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Matches 215;
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Fax: +55-11-3091-2186
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                                                                                   SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGATAGAAATCAATGACCTCAAGAAATCTTTTGGCGTTCGGATCTTATGGCAAGGTCTC
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                                                  Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo
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Western X phytoplasma
Western X phytoplasm
Westerna; Firmicutes; Mollicutes; Acholeplasmatales;
Acholeplasmataceae; Phytoplasma; 16SrIII (X-disease group)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 75.2; DB 14;
Pred. No. 2.4e-12;
0; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Schistosoma mansoni"
/mol type="mRNA"
/db_xef="taxon:6183"
/clone="Mil-0091T-L258-D10.B"
/sex="mixed pool"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="miracidium"
/dev_stage="miracidium"
/clone_lib="ML1-0091"
/note="Vector: pGEM T-easy"
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                          Departamento de Bioquimica
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Matches 155; Conservative
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Best Local Similarity
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Capsicum annuum
Eukaryotu, viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Capsicum.
I (bases I to 668)
Richins, R., Alvarado, K., Leger, J. and O'Connell, M.A.
Richins, R., Alvarado, K., Leger, J. and Connell, M.A.
Responsive transcripts in Phytophthora capsici-challenged roots of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 GGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGA 417
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 ATTGCAATTGCAAGGGCCATATTGAAGAATCCAAGAATCCTTCTTCTTGATGAAGCAACA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGAC 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 AGTGCATTGGATGCTGAGTCTGAACGTGTTGTTCAAGAAGCATTGGAAAAGTTATGACA 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="mth2"
/note="Vector: pBeloBAC11; Site 1: HindIII; Site 2: HindIII; Cook, D.R. and Kim, D.\overline{\mathbf{J}}, unpublished"
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                                                                                                                                                                                                      9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
Contact: O'Connell, MA
Department of Agronomy and Horticulture
New Mexico State University
MSC 30, P.O. Box 30003, Las Cruces, NM 88003, USA
Tel: 505 646 5172
                                                                            Town,C.D., Shetty,J., Koo,H. and Feldblyum,T.F. Sequencing of BAC ends from Medicago truncatula Unpublished (2003)
Cher GSSs: MEEBP1OTR
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                           1. .639
/organism="Medicago truncatula"
/organism="Medicago truncatula"
/mol type="genomic DNA"
/cultivar="genotype A17"
/db xref="taxon:3880"
/clone="20B20"
                                                                                                                                                                                                                                                               Email: cdtown@tigr.org
Seg primer: TGTAAAACGACGGCCAGT
Class: BAC ends.
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CA847456.1 GI:26997386
                                     Medicago.
1 (bases 1 to 639)
                                                                                                                                                                                                                              Tel: 301-838-3523
Fax: 301-838-0208
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1 (bases 1 to 4010)
Min, W., Lillehoj, H.S., Ashwell, C.M., Matukumalli, L.K., van Tassel, C. and Han, J.Y.
Chicken intestinal lymphocyte EST database as a resource for the analysis of mucosal immune function
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'clone lib="CM334 Root cDNA"
'note="Organ: Root; Vector: Zap; Site_1: EcoR1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 Arrigicariogoangadaarintraaaagariceaceeararracrigitadargaaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 GGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 gercraeacaccarecraeacaacareeaacreeaacrreaacrreaereegecaaaacaaaca
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                                                                                                                                                                                                                                                                    /organism="Capsicum annuum"
/mol_type="mRNA"
/strain="Criollo de Morelos 334 (CM334)"
/db_xref="taxon:4072"
/clone="R529-81"
/dev stage="6 hours after Phytophthora capsiciinoculation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 668;
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llarity 56.7%; Pred. No. 3.4e-08;
Conservative 0; Mismatches 88;
Fax: 505 646 6041
Email: moconnel@nmsu.edu
Seq primer: 73
High quality sequence stop: 66
Location/Qualifiers
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Gallus gallus (chicken)
Gallus gallus
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/clone lib="igal - Chicken Intestinal Lymphocyte"
/note="Organ: Intestine; Vector: pCMV-SPORT6; Site 1:
Sall; Site 2: Not1; Normalized library from chicken gut
infected with poccidia duodenum and middle gut."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Frazer Murray
Dept. Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
/tissue_type="Gut"
/cell_type="Lymphocyte"
/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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ilarity 60.6%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                         417
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Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt '' -trim_fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 GGATTTGACACTGTAGTTGGAGAAAAAGGCATTCTACTTTCAGGTGGACAGAAAGCAGCGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 ATTGCAATTGCTCGAGCTCTGCTCAAGAATCCCAAAATTCTTCTGTTAGACGAAGCAACA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Eukaryote, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves; Neognathae, Galliformes; Phasianidae;
Phasianinae, Gallus.
I bases 1 to 542)
Min, W., Lillehol, H.S., Ashwell, C.M., Matukumalli, L.K., van
Tassel, C. and Han, J.Y.
Chicken intestinal lymphocyte EST database as a resource for the
analysis of mucosal immune function
Unpublished (2003)
                                                                                                                                                                                                    /clone lib="1GAL - Chicken Intestinal Lymphocyte"
/note="Organ: Intestine; Vector: pCMV-SPORT6; Site 1:
Sall; Site 2: Not1; Normalized library from chicken gut
infected with coccidia duodenum and middle gut."
                                                                                                                                                                                                                                                                                                                                                                                                           358 GGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGA
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       478 GGAGCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 agrecrecarecreaaaarcagraccragrecaagaacrere 253
                                                                                                                                                                                                                                                                                                                                                                Indels
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Animal Parasite Diseases Laboratory
Animal and Natural Resources Institute, USDA
Bldg 1043, BARC-East, Beltsville, MD 20705, USA
Tel: 3015048771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Gallus gallus"
/mol_type="mRNA"
/strain="white leghorn SC"
/db_xref="taxon:9031"
/clone="1GAL_38A17"
/sex="mixed"
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    organism="Gallus gallus"
                                                                                                                   /tissue_type="Gut"
/cell_type="Lymphocyte"
/dev_stage="Adult"
/lab_host="EMDH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 542.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :e: 38 row: A column: 17 primer: ATTTAGGTGACACTATAG
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Matches 100;
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DEFINITION
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CD731492
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AL586817 Stratagene Chick Embryo Lambda cDNA Library (* 937405)
Gallus gallus cDNA clone ROS048G05, mRNA sequence.
AL586817.1 GI:13191851
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                                                                                                417
                                                                                                                                                 329
                                                                                                                                                                                                                          /note="Vector: pBLUBSCRIPT SK; Site_1: BcoR1; Site_2: Xho1; Cloned unidirectionally. Primer: Oligo dT. Uni-ZAP XR vector. Average insert Size: 1.5kb.; 5' adaptor sequence: 5' GAATTCGGCACGAG 3'; 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .619
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/ tissue_type="mmxno"
/ dev_stage="5 days old"
/ lab_host="Solk cells (kanamycin resistant)"
/ clone lib="Stratagene Chick Embryo Lambda cDNA Library 937405"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1. (Dases 1 to 619)
                                                                                                     GGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGTGGTGGCGAACAACAACGA
                                                                                                                                                 270 GGATTTGACACTGTAGTTGGAGAAAAAGGCATTCTACTTTCAGGTGGACAGAAGCAGGA
                                                   Gaps
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     Length 542;
                                                                                                                                                                                                                                                                                                478 GGAGCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTG 522
                                                                                                                                                                                                                                                                                                                                            390 agrecrergadahangaeraceragiesagaheeree 434
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                                                   65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stratagene Chick Embryo Lambda cDNA Library
Unpublished (2001)
Score 61; DB 14;
Pred. No. 7.5e-08;
0; Mismatches 65;
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/done liberCESECHN64"
//orde="Organ: whole embryo; Vector: pBluescript II KS(+);
Site_1: BCORI, Site_2: Not!; This normalized library was
constructed from I million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand synthesis reaction.
Following this first strand synthesis reaction.
Following this first strand synthesis reaction.
Following this first strand synthesis reaction.
Following this first strand synthesis reaction.
Following this first strand synthesis reaction.
Following this first strand synthesis double-stranded
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianinae; Gallus.
1 (bases 1 to 798)
Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W. T., Tickle, C., Erown, W. R. A., Wilson, S. A. and Hubbard, S. J.
Courte, Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                     BU328328 1798 bp mRNA linear EST 28-NOV-2002 603496289F1 CSEQCHN64 Gallus gallus cDNA clone ChEST406a24 5', mRNA
358 GGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGA 417
                                               162 gdarrirgacacreradregagaaaaaggcarrcracrirrcaggregacagaagggg 221
                                                                                                        358 GGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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University of Manchester Institute of Science and Technology
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                                                                                                                                                                                                                                                                         282 agracicirgangergaaangagraceragracaagaacererg 326
                                                                                                                                                                                                                      478 GGAGCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTG 522
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/organism="Gallus gallus"
/organism="Gallus gallus"
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/strain="Mhite Leghorn, Hisex"
/db_xref="taxon:9031"
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/tissue_type="whole embryo"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PO Box 88, Manchester, M60 1QD, UK
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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BU328328
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//dev stage="adult"
/lab_hose="bH10B"
/clone=lb="CSEQCHNSB"
/notoe="Organ: small intestine; Vector: pBluescript II
/notoe="Organ: small intestine; Vector: pBluescript II
/S(+); Site_1: EcoRI; Site_2: Not1; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Archosauria; Basianidae; Phasianinae; Gallus.

1 (bases 1 to 743)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. Curr. Biol. 12 (22); 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                             BU399305 7-NOV-2002 743 bp mRNA linear EST 27-NOV-2002 603535206F1 CSEQCHN58 Gallus gallus cDNA clone ChEST49511 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                          417
                                                                          176 GGATTTGACACTGTAGTTGGAGAAAAGGCATTCTACTTTCAGGTGGACAGAAGCAGCAG
                                                                                                                                   ATTGCAATTGCTCGAGCTCTGCTCAAGAATCCCAAAATTCTTCTTGTTAGACGAAGCAACA 295
                       GGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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                                                                                                                                                                                                                                              478 GGAGCICTAGAITTAACAAACAGTGAGCTAGICATAGAAGCATTG 522
                                                                                                                                                                                                                                                                                                    296 AGTGCTCTGGATGCTGAAATGAGTACCTAGTGCAAGAAGCTCTG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Gallus gallus"
mol_type="mRNA"
/errain="Compton Line 151"
/db xref="taxon:901"
/clone="ChEST49511"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
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Email: Simon.Hubbard@umist.ac.uk.
Encation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
BU399305
BU399305.1 GI:25768361
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Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .743
                                                                                                                                                                                        236
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VERSION
KEYWORDS
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COMMENT
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AUTHORS
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BU399305
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/dev_stage="22"
/lab_host=="hilds"
/lab_host=="hilds"
/lab_host=="hilds"
/lab_host=="hilds"
/clone lib="CSEGGHI14"
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ECORI; Site 2: Not1; Modification of pBluescript II KS[+)
(Stratagene] Vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from massenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and ECORI.
Ligate in double stranded adaptor containing Bsg1 and
BamHI sites [5'gagccggggagccggaccggatccgaaaaaaag]
[5'aattcttttttcggatccggggctggaccgg]
                                                                                                                                                                                                                                                                                                                                                                                                    BU112595 907 bp mRNA linear EST 25-NOV-2002 603129071F1 CSEQCHL14 Gallus gallus clone ChEST102n17 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 GGTCTTGAGTCGTTCGAGGAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 ggartrigacacrgradriggagaaaaággcarrcracrricaggiggacagaagcagdga 453
                                                                                                                    222 ATTGCAATTGCTCGAAGCTCTGCTCAAGAATCCTCAAAATTCTTCTGTTAGACGAAGCAACA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

( basea 1 to 907)

Boardman, P. B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                     GGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAA
                                                                   162 GGATTTGACACTGTAGTTGGAGAAAAAGGCATTCTACTTCAGGTGGACAGAAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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                                                                                                                                                                                                                          478 GGAGCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTG 522
                                                                                                                                                                                                                                                                           282 adrecriciedargereaaangagraccradigeaadaadcrerd 326
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60.6%; Pred. No. 9.4e-08;
tive '0; Mismatches 65;
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/mol_type="mRNA"
/strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PO BOX 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon. Hubbard@umist.ac.uk.
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BU112595.1 GI:25316826
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Gallus gallus
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//done lib="CSENCENNS9"
//done lib="CSENCENNS9"
//done lib="CSENCENNS9"
//done="Organ: limbs; Vector: pBluescript II KS(+); Site_1:
ECORI, Site_2: Not1; This normalized library was
constructed from limilion independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BU407162 896 bp mRNA linear EST 27-NOV-2002 603484011F1 CSEQCHN59 Gallus gallus cDNA clone ChEST375f3 5', mRNA
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                                                                                                                            452
Eukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 896)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, J. Frong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                               478 GGAGCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGAC
                                                                                                                                                                                                                                453 AGTGCTCTGGATGCTGAAAATGAGTACCTAGTGCAAGAAGAGCTCTGGACCGGCTGATGGCA
                                                                                                                         393 ATTGCAATTGCTCGAGCTCTGCACAAATCCCAAAATTCTTCTGTTAGACGAAGCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                   AAAGGCGCCACCGTTGTTGCTACGCACTCGCCCCTCTTCCGAGAAT 586
                                                                                                                                                                                                                                                                                                                                 AGGGAGGACAGTCTTAATCATCGCTCACCGTCTGTCTACTATTCAGAAT 561
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llarity 60.6%; Pred. No. 9.4e-08;
Conservative 0; Mismatches 65;
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/strain="White Leghorn, Hisex"
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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/clone="ChEST375f3"
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/lab_host="DH10B"
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Gallus gallus (chicken)
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S Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
L Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall (UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu/
for details.
                                                                                                                                    BQ865169 759 bp mRNA linear BST 14-AUG-2002 QGC28024.yg.abl QG_ABCDI lettuce salinas Lactuca sativa cDNA clone QC2020024, mRNA sequence.
BQ865169 GI:22250634
                                                                                                                                                                                                                      Lactuca sativa. Activa. Embryophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Eukaryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
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.larity 58.2%; Pred. No. 1.3e-07;
Conservative 0; Mismatches 76; Indels 0;
                                           478 GGAGCICTAGATITAACAAACAGIGAGCTAGICATAGAAGCATIG 522
                                                                 514 AGIGCICIGGAIGCIGAAAAIGAGIACCIAGIGCAAGAAGCICIG 558
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 576)
8 Sasaki, T. and Yamanoto, K.
Rice CDNA from mature leaf (2000)
Unpublished (2000)
Contact: Takkuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-6602, Japan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AU090519 Fice mature leaf Oryza sativa (japonica cultivar-group) cDNA clone S20717, mRNA sequence.
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                                                                                                                                                                                                                  305-8602, Japan
Tel: 81-296-38-7441
Fax: 81-298-38-7468
Emall: tssaski@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = RQP'.
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468 TGAAAGCTCCTCCTATTTTGCTGTGTGATGAAGCAACAAGTGCTCTGGATAGCACAACAG
                                                                                                                                   500 GTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGACAAAGGCGCCACCGTTGTTG
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9.8%; Score 59.4; DB 9; Length 576;
Best Local Similarity 55.6%; Pred. No. 2.5e-07;
Matches 114; Conservative 0; Mismatches 91; Indels C
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| Organism="Oryza sativa (japonic | Arganism="Oryza sativa (japonic | Vype="mRNA" | Alipponbare" | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponic | Alipponi
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306 AGAAAGAACCACACTCGTTGTCGCT 330
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358
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                                                     ORGANISM
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BF700602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 AATCCCAAAATTCTTCTCCTAGATGAAGCAACCAGTGCGCTGGATGCCGAAAATGAGTAC 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                        Email: estewatson.wustl.edu
High quality sequence stops: 315
Source: IMAGE Consortium, binn.
This clone is available royalty-free through Lini; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP1
High quality sequence stop: 315.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 CTAGICATAGAAGCAITGAGAGCACICGCCGACAAAGGCGCCCACCGTIGTIGTIGC 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                         1 (bases 1 to 358)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Hollnan, M., Hultman, M., Kucaba, T., Le, M., Lennon, C., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch al Similarity 58.5%; Pred. No. 2.3e-07; S. Servative 0; Mismatches 73; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="GDB:377235s"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:203224"
 ARABIDOPSIS ;, mRNA sequence.
                                                                                                                                                                                                                                                 The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                      Homo sapiens (human)
                   H54613
H54613.1 GI:995139
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                                                                                          Homo sapiens
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DEFINITION

ACCESSION

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/Lissue type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC_56"
/note="Crgan: brain: Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggocgcctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded CDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTARGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGCGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 426)

E 1 (bases 1 to 426)

I Unpublished (1999)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov
Tissue Procurement: ArCc

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Plate: LLCM1120 row: h column: 20

High quality sequence stop: 426.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .426
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4285507"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: July 30, 2004, 14:14:26
BF700602.1 GI:11986010
                                                                                    Homo sapiens (human)
                                                                                                                                       Homo sapiens
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein

July 27, 2004, 16:28:59; Search time 54 Seconds (without alignments) 1062.169 Million cell updates/sec Run on:

US-09-868-338-9 1019 1 MIEINDLKKSFGVRILWQGL......VVVATHSPLFRESADTIIKL

score: Title: Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues Searched:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SUMMAKIES		
Result No.	Score	Query	Length	DB	ΩI		
-	1019	100.0	203	!	AAB12592	Aab12592 Brevibact	
71	408	40.0	213	9	ABU01071		
e	σ	39.2	213	9	ABU02491	ς. Ω	
4	399		213	ø	ABP81472	Abp81472 Streptoco	
S	æ		213	9	ABU00443	ς Ω	
9	385	37.8	213	~	AAW80649	Aaw80649 S. pneumo	
7		37.3	210	9	ABU02461	Abu02461 S. pneumo	
8		37.3	210	9	ABP81469	Abp81469 Streptoco	
σ	373	36.6	211	S	ABB53309	6	
10	362.5	35.6	465	9	ABU36156	Abu36156 Protein e	
11		'n.	258	4,	AAU45701	Aau45701 Propionib	
12	S	35.2	258	9	ABM42220	Abm42220 Propionib	
13	S	34.6	270	2	ADC97592	Adc97592 E. faeciu	
14			466	9	ABU35504	Abu35504 Protein e	
15	'n	34.5	237	Ŋ	ABP26089		
16	348	34.2	250	Ŋ	ABP26471		
17	•	•	227	9	ABU39077	7	
18	344	33.8	207	Ŋ	ABB49925	Abb49925 Listeria	
19	344		219	N	AAY34450	Aay34450 Porphorym	
20	344	33.8	238	N	AAY34327	Aay34327 Porphorym	
21	343	33.7	224	Ŋ	ABP26472		
22	339.5	33.3	222	4	AAB76730	0	
23		33.3	222	4	AAG90702	Aag90702 C glutami	
24	339	33.3	259	ß	ABB55099		
25	339	33.3	648	4	AAU38402	Aau38402 Salmonell	

Abb47488 Listeria Abu16155 Protein e Abu16155 Protein e Abu17284 Straphyloc Aau17113 Straphyloc Aau17113 Staphyloc Aau86648 S. pneumo Abb52928 Escherich Abb48879 Listeria Abu2213 S. pneumo Abu2223 S. pneumo Abu2225 Brotein e Abp33755 Staphyloc Adb12657 Alloiococ Adb12657 Alloiococ Adb12657 Alloiococ Abb54027 Iactococc Abb59241 Microbial Ebu1621
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AL IGNMENTS

AAB12592 standard; protein; 203 AA. (revised)
(first entry) 12-SEP-2003 09-NOV-2000 AAB12592; RESULT 1

Brevibacterium lactofermentum gltBD ORF2 protein SEQ ID NO:9.

Brevibacterium lactofermentum; ABC transporter; breeding; ATPase; corynebacterium; gltBD; L-glutamic acid.

Corynebacterium glutamicum

WO200037647-A1.

29-JUN-2000.

99WO-JP007079. 16-DEC-1999;

(AJIN) AJINOMOTO CO INC

98JP-00360621.

18-DEC-1998;

Nakamatsu T; Matsui K, Kanno S, Kimura E,

WPI; 2000-452189/39. N-PSDB; AAA65395.

ABC transporter constituent of Brevibacterium lactofermentum, its encoded gene and variants, applicable in breeding Corynebacteria particularly for production of L-glutamic acid.

Claim 5; Page 30-31; 34pp; Japanese.

The present invention describes a protein (I) which can be used to construct an ATP binding cassette (ABC) transporter. ABC transporter DNAs can be used in breeding Corymbbacteria particularly for production of L-glutamic acid. The present sequence represents an ORF (open reading frame) protein from the Brevibacterium lactofermentum gitBD gene, which is used in the exemplification of the present invention. (Updated on 12-SEP-2003 to standardise OS field)

Sequence 203 AA;

Query Match

Length 203; 100.0%; Score 1019; DB 3;

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(revised)
(first entry)
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(GENO-) INST GENOMIC RES.
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N-PSDB; ABX07781.
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Best Local Similarity
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11-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the expecification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein. DNA or antibody in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                              EDVDLIKLSTRKORLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQVLHAVG 120
                                                                                                                                                                                                                                                   LESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEALRALADK 180
                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media cear infection.
                                                                                                                                                                                              BDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQVLHAVG
                                                                   1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV
                                                                                                MIEINDLKKSFGVRILMOGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSGQILV
                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S. pneumoniae type 4 strain protein from coding region #642
                        Indels
  ; Pred. No. 1.1e-103; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae; type 4 strain
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                                                                                                                                                                                                                                                                                                                                             GATVVVATHSPLFRESADTIIKL 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU01071 standard; protein; 213 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser
                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.0%;
Matches 203; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-2002; 2002WO-IB002163.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-040579/03.
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11-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                           181
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the target sequence, and where the parts of the primers having
consistential complementarity define the termini of the target sequence to
be amplified, assay comprising contacting a test compound with the
contacting and determining whether the test compound binds to the protein
and a Streptococcus pneumoniae bacterium, where one or more genes
concoling the proteins has been rendered inactive. The proteins, nucleic
concoling the proteins has been rendered inactive. The proteins, nucleic
concoling the proteins disease or infection due to streptococcus
controlled, antibody and compositions are useful as medicaments for
treating or preventing a disease or infection due to streptococcus
controlled, particularly S. pneumoniae, such as preumonia, sepsis, oitis
media or ear infection. They are also useful in developing vactines,
diagnostics and antibiotics. The methods are useful for identifying
confimunodominant proteins. The present sequence is one of the 2469 proteins
contact the sequence data for this patent did not form part of the printed
contact price of the printed proteins at ftp. wipo.int/pub/published_pot_sequences. (Updated on 23-OCT-2003 to
standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 BDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKWPEIPQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MIELKNISKKFGSRQLFSDMNLHPEGGKIYALIGTSGCGKTTLLNMIGRLEPYDKGQIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DGTSLKDI---KPSVPFRDYLGYLFQDFGLIESQTVKENLNLGLVGKKLKEKEKISLMKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MIEINDLKKSFGVRILMQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. pneumoniae type 4 strain protein from coding region #2069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.0%; Score 408; DB 6; Length 21
41.9%; Pred. No. 3e-36;
tive 44; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :|: | :|::|||:|| | :|::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 LRALADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae; type 4 strain.
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constitution and are set an antibody which binds one of the proteins. Treating appearing a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nuclectides 8-100 of a sequence not defined in the specification, for amplifying a target composition in the specification, for amplifying a target to sequence not defined in the specification, for amplifying a target companies in the specification, for amplifying a target sequence contained within a Streeptococcus nucleic acid sequence, the first primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having conditions assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus caid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2469 proteins expressed by the identified coding regions from the genomic sequence. Note: The sequence data for this parent did not form part of the printed expectivitation, but was obtained in electronic format directly from NIPO or at fitp.wipo.int/pub/published_pot_sequences. (Updated on 23-OCT-2003 to standardise OS field)
                       New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
                                                                                                                                                                                                                                          The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the
                                                                                                                                                                              Claim 1; SEQ ID NO 4138; 56pp; English.
                                                                                                                        ear infection
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-LESFE-----EKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173 61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHXWPEIPQVLHAVG 120 1 MIDIOGLEKKRUDRAIFSGLNLKLEKGKVYALIGKSGSGKTTLLNILGKLEKIDGGRVLY 60 1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60 Query Match 39.2%; Score 399; DB 6; Length 213; Best Local Similarity 42.9%; Pred. No. 2.9e-35; Matches 90; Conservative 40; Mismatches 70; Indels 10; Gaps 174 LRALADKGATVVVATHSPLFRESADTIIKL 203 LVDLKDENRIIIIATHNPLVWNKADBIIDM 207 Sequence 213 AA; 121 178 g g d ò ò 유 à ò

Streptococcus pneumoniae; infection; otitis media; antibacterial; Streptococcus pneumoniae polypeptide SEQ ID NO 389. ABP81472 standard; protein; 213 AA (first entry) ABP81472; ABPR1472
ID ABPR
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XX RESULT

a Streptococcus pneumoniae genomic sequence, a fragment or degenerate variant of the polynuclectide or a nucleic acid sequence 95% identical to one of the polynuclectides. The S. pneumoniae polynuclectides and encoded polypeptides (ABPB1299-ABPB1674) are useful for treating or preventing S pneumoniae infections or non-systemic diseases, e.g. ottiss media, which are induced or exacerbated by S. pneumoniae. These are also useful for detecting S. pneumoniae in a biological sample or diagnosing S. pneumoniae in a subject. The polynuclectides have antibacterial activity and are useful in gene therapy EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQVLHAVG 120 121 -LESFE-----EKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173 1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60 The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) 10; Gaps New Streptococcus pneumoniae polynucleotides, useful for treating or preventing S. pneumoniae infections, or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. Russell DP; Length 213; 39.2%; Score 399; DB 6; Length 213 42.9%; Pred. No. 2.9e-35; iive 40; Mismatches 70; Indels Chakravarti DN, 174 LRALADKGATVVVATHSPLFRESADTIIKL 203 Claim 42; Page 642-643; 1091pp; English Green BA, 2001US-0283948P. 2001US-0284443P. L2-APR-2002; 2002WO-US011524. (AMCY) AMERICAN CYANAMID Local Similarity 42.9 es 90; Conservative Streptococcus pneumoniae. diagnosis; gene therapy. Zagursky RJ, Masi AW, WPI; 2003-093010/08. N-PSDB; ABZ42320 Sequence 213 AA; WO200283855-A2. 16-APR-2001; 18-APR-2001; 24-OCT-2002 Wooters JL; Query Match Best Loc Matches à a ò 임 ठ g à

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 S. pneumoniae type 4 strain protein from coding region #10. (revised)
(first entry) 23-OCT-2003 11-FEB-2003 ABU00443;

Ā

ABU00443 standard; protein; 213

Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;

antiinflammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.

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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable formath, or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the specification (available on a computer readable formath, or its fragment, corpressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS5654. Also included are an antibody which binds one of the proteins, Creating a patient by administering the protein. DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid eaduence of the first primer is substantially complementary to the target sequence, and where the specification, for amplifying a target the target sequence, and where the parts of the primers having substantially complementary to the target sequence or and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having substantial complementary of the primers having contacting a streptococcus pneumoniae bacterium, where one or more genes encoding the protein and determining whether the test compound with the protein, and determining and contacting a test compound with the conding the proteins has been rendered inactive. The proteins, neclain or preventing a disease or infection due to streptococcus conding the proteins and antibiotics. The methods are useful for identifying the media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying expense of immunodominant proteins. The present sequence is one of the 2469 proteins expressed by the identified coding regions from the genomic sequence. Note: The sequence data for this patent did not form part of the printed of the sequence is one of the printed of the protein of the printed of the protein of the printed of the p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDVDLLKLSTRKORLYRKNTVGYLFODYALIPDRTVKFNLQLAV-----EKHKWPEIPQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media c
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                                                                    Streptococcus pneumoniae, type 4 strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 20; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 Fraser C;
                                                                                                                                                                                                            27-MAR-2002; 2002WO-IB002163.
                                                                                                                                                                                                                                                             27-MAR-2001; 2001GB-00007658.
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                                                                                                                                                                                                                                                                                                          (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-040579/03
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Best Local S
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This sequence represents a Streptococcus pneumoniae transport protein. The invention provides DNA sequences (AAV65201 to AAV6534) from the Streptococcus pneumoniae genome and corresponding protein sequences (AAW80728). The protein sequences are classified as hypothetical, cell wall biosynthetic, external target, or minimal gene ext proteins. A recombinant host containing a vector comprising any of the above nucleic acids can be used for the recombinant expression of the proteins. The invention also provides a DNA chip having arrayed on it at last 15 hase pair fragment of any one or more of these DNA sequences. The DNA chip can be used methods for evaluating gene expression in S. pneumoniae and for identifying virulence genes in S. pneumoniae. The although the selective of the provention or peptide fragments can be used to treat S. pneumoniae infection. The antibodies can also be used to detect S. pneumoniae cells
                    Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip; virulence; antibody; infection; detection; treatment; hypothetical; cell wall biosynthetic, external target; minimal gene set protein.
115 VIHAVGLESFEEKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIEAL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae nucleic acid sequences - used in DNA chips for evaluating gene expression, and identification of virulence genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skatrud PL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MIELKNITKTIGGKVILDNISLRIDQGDLVAIVGKSGSGKSTLLNLLGLIDGDYSGRYEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.8%; Score 385; DB 2; Length 213; 39.7%; Pred. No. 1e-33; Live 46; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jaskunas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dehoff BS, Hoskins JA, Jaskunas
Peery RB, Rockey PK, Rosteck PR,
J, Treadway PJ, Young Bellido ML;
                                                                                            RALADKGATVVVATHSPLFRESADTIIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 236-237; 333pp; English.
                                                                                                                                                                                                AAW80649 standard; protein; 213 AA
                                                                                                                                                                                                                                                                                                        S. pneumoniae transport protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US022578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0036281P.
                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Solenberg PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burgett SG,
Norris FH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIL ) LILLY & CO ELI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 213 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-DEC-1996;
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Mills BJ,
Smith MC,
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Matches
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61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKWPEIPQ 114

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6; Gaps

9

sepsis, otitis

particularly S. pneumoniae, such as pneumonia,

us-09-868-338-9.rag

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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as Streptococcus pneumoniae type 4 strain genomic sequence appearing as treating a patient by administering the protein, binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the complete acid edefined in the specification, for amplifying a target sequence ontained within a Streptococcus nucleic acid sequence, the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the target sequence of the target sequence, and where the parts of the primer shaving substantially complementary to the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes cond molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus
New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
                                                                                                 VLHAVGLESFEEKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIEAL 174
                                                                                                                                                Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumoniae type 4 strain protein from coding region #2039.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae; type 4 strain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU02461 standard; protein; 210 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-2001; 2001GB-00007658.
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INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-040579/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2002.
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         media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2469 proteins expressed by the identified coding regions from the genomic sequence. Note: The sequence data for this patent did not form part of the printed at ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                      114
                                                                                                                                                                                                                                                                                                     60 RGKD---LANYKSSDFFRHELGYLFONFGLIENOSIEENLKLGLIGOKLSRSEORLROKO 116
                                                                                                                                                                                                                                                                                                                                                             117 ALEQVGLVYLDLDKRIFELSGGESQRVALAKIILKNPPFILADEPTASIDPATSQLIMEI 176
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                                                                                                                                                                                                                             1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV
                                                                                                                                                                                                                                              61 EDVDLIKLSTRKORLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEI-----PQ
                                                                                                                                                                                                                                                                                                                                            115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) a Streptococcus pneumoniae genomic sequence, a fragment or degenerate
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for treating or diseases, e.g. pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Russell DP;
                                                                                                                                                                                                  11;
                                                                                                                                                                     Length 210;
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Streptococcus pneumoniae polynucleotides, useful preventing S. pneumoniae infections, or non-systemic otitis media, which are induced or exacerbated by S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae polypeptide SEQ ID NO 386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chakravarti DN,
                                                                                                                                                                    37.3%; Score 380.5; DB 6;
41.0%; Pred. No. 3.1e-33;
iive 41; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                     174 LRALADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 42; Page 637-638; 1091pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-2001; 2001US-0283948P.
18-APR-2001; 2001US-028443P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                  86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Masi AW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003-093010/08.
                                                                                                                                                                                    Similarity
                                                                                                                                          Sequence 210 AA;
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ABP81469
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variant of the polynucleotide or a nucleic acid sequence 95% identical to one of the polynucleotides. The S. pneumoniae polynucleotides and encoded polypeptides (ABP81299-ABP81674) are useful for treating or preventing S. pneumoniae infections or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. These are also useful for pneumoniae in a biological sample or disgnosing S. pneumoniae in a biological sample or disgnosing S. pneumoniae in a biological sample or disgnosing S. activity and are useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 RGKD---LANYKSSDFFRHELGYLFQNFGLIENQSIEENLKLGLIGGKLSRSEQRLRQKQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEI-----PQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MIBINDLKKSFGVRILWQGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MIELKQVSKSFGERELFSNLSMIFEAGKVYALIGSSGSGKTILMMMIGKLE-PYDGTIFY
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                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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                                                                                                                                                                                                                                                                                                                          Ehrlich SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRALADKGATVVVATHSPLFRESADTIIKL 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis; IL1403
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                Sequence 210 AA;
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16-MAY-2002
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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                174
                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense, prokaryotic essential gene, cell proliferation, drug design.
     equivalent
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Xu HH;
                                                                                                                                                          1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV
                                                                                                                                                                                                                            EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKWPEIPQ
                                                                                                                                                                                                                                                                115 VIHAVGLESFEEKPVFELSGGEQORTALARVILKNPRIILADEPTGALDLTNSELVIEAL
                                            9
                                                                                                                                    Gaps
                                          (Updated on 29-AUG-2003
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cheese. Note: The sequence data for this patent is based on eq patent WO200177334 (published 18-OCT-2001) which is available electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2 standardise OS field)
                                                                                                        Length 211;
                                                                                                                                  Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein encoded by Prokaryotic essential gene #21683.
                                                                                             36.6%; Score 373; DB 5; Lk
39.2%; Pred. No. 2.1e-32;
wiematches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 64080; 1766pp; English.
                                                                                                                                                                                                                                                                                                                    RALADKGATVVVATHSPLFRESADTIIKL 203
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                                                                                                                                                                                                                                                                                                                                                                                                              ABU36156 standard; protein; 465
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US-00815242.
2001US-00948993.
2001US-0342923P.
2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002WO-US009107.
                                                                                                                       Local Similarity 39.2 tes 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2003-029926/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ACA40026.
                                                                                  Sequence 211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2001; 2
06-SEP-2001; 2
25-OCT-2001; 2
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                                                                                                           Query Match
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Wall D,
                                                                                                                          Best Loc
Matches
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encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that has an activity against a biological pathway to proliferation or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the colliferation of an organism. The antisense nucleic acids required for callular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for cellular proliferation to inverse the propose in acids drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of K. pneumoniae or P. aeruginosa. The present sequence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
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Sequence 465 AA;

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IIBLKNVYKYITNGVTTNAVLKGIDLKLKAHDFIVILGPSGSGKTTLLNIISGMDRPSSG 290
                                                                                                                                                      57 QILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPE----I 112
                                                                                                                                                                              113 POVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKAPRIILADEPTGALDLTNSELVIE 172
                                                                                                                                                                                                                                                    351 DELLEAVGMKHLQKKLPNELSGGQQQRVSIARAFAKNPILIFGDEPTGALDLEMTQIVLK 410
                                                                              1 MIEINDLKK--SFGV--RILWOGLSHKFLPGTMTALIGASGSGKSTLLNCLGTLDKPSSG
                                               Gaps
                                           ο.
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         Length 465;
                     ,9e-31;
... 70; Indels
     35.6%; Score 362.5; DB 6; 36.7%; Pred. No. 9.9e-31; iive 54; Mismatches 70;
                                                                                                                                                                                                                                                                                                                           411 QFLAIKQRYKTTWVIVTHNNLIAQLADLVI 440
                                                                                                                                                                                                                                                                                                       173 ALRALADK-GATVVVATHSPLFRESADTII 201
Ouery Match
Best Local Similarity 36.7,
Watches 77, Conservative
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AAU45701 standard; protein; 258 AA (first entry) 27-FEB-2002 AAU45701; RESULT 11

Propionibacterium acnes immunogenic protein #6597.

SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant

Propionibacterium acnes

WO200181581-A2

01-NOV-2001.

20-APR-2001; 2001WO-US012865

Propionibacterium acnes transporter-related polypeptide #6896

(first entry)

20-OCT-2003

ABM42220;

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ABM42220 standard; protein; 258

RESULT 12

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orquences Arobson's taplescine recipies Linear certum actual and organizations and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPPO syndrowits, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lessons associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention of determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by this patent did not form part of the printed specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 V----LHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSEL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGQILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 GGSIVASGVSHNFSTTHNRNLVLDDVTVSMQPGVMTLLEGVSGSGKTTLLNIMSGLLKPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LPGTMTALTGASGSGKSTLLNCLGTLDKPS
                                                                                                                                                                                                                                                                               Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.2%; Score 359; DB 4; Length 258; 40.5%; Pred. No. 9.9e-31; tive 36; Mismatches 65; Indels 2
                                                                                                                                                   Wang SS, Bhatia A;
                                                                                                                                                Mitcham JL, Wang Si
Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 VIEALRALA--DKGATVVVATHSPLFRESA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 VFELLRALAEDEKGRTVVLSSHDPTAKEYA 243
                                                                                                                                                                                                                                                                                                                                                                    Claim 3; SEQ ID NO 6896; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published pct sequences
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                  21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                Persing DH, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                             treating acne vulgaris.
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                                                                                                       (CORI-) CORIXA CORP
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es 85; Conserv
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154 VMAIEALERVGIAHLQDRYPRQLSGGEAQRVGIARAIAGDRPILLADEPTGQLDRRNSQM 213

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KW Acne immun KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200 KW WO 200
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Acre vilgaris; antiseborrhoeic; dermatological; antibacterial; immunossimulant; immune response; vaccine.

Propionibacterium acnes.
W02003033515-A1.
24-APR-2003.
11-OCT-2002; 2002W0-US032727.
15-OCT-2001; 2001US-00978825.
(CORI-) CORIXA CORP.
Mitcham UL, Skelky YAW, Persing DH, Bhatia A, Maisonneuve UL;
Lang Y, Wang S, Jen S, Lodes WJ, Benson DR, Jones R, Carter D;
Barth B, Vallieve-Douglass J;
NPFSDB; ACR64455.
Ne PSDB; ACR64455.

Ne PSDB; ACR64455.

Ne PSDB; ACR64455.

Claim 3k; SEQ ID NO 6896; 1481pp; English.

Claim 3k; SEQ ID NO 6896; 1481pp; English.

The invention relates to an isolated polymucleotide (ACR64435-ACR64733) encoding the polypeptides encoding acne vulgaris, or for stimulating an immune acnes protein.

Claim 3k; SEQ ID NO 6896; 1481pp; English.

The invention relates to an isolated polymucleotide (ACR64435-ACR64733) encoding the polypeptides encoded by the polymucleotides (BMB36624-ABW64356) and to immunogenic fragments of P. acnes polypeptides. The invention as an isolated or calls comprising a polypeptide of the invention; an immune response specific for a P. acnes polypeptide of the invention; an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising P. acnes polypeptides, antibodies, fusion proteins. T cell populations, or antibodies, antibodies, fusion proteins compositing P. acnes in a method for stimulating cells that express the polypeptide); a method and an isolated presence or absence of P. acnes in a patient, mad a method for inhibiting the presence or absence of P. acnes in a patient, mad and an active conversion or polymerial patient; and a method for inhibiting the presence or absence of P. acnes in a patient, mad and an accompaniant or polymerial patient and an encoded patient and an active profession or proteins or polymerial patient and an encoded patient and an encoded patient and an encoded patient and an encoded patient and an encoded patient and an encoded patient anot be accompaniant and an encoded patient and an encoded patient

The invention relates to an isolated polymuclectide (ACF64435-ACF64733)
encoding a Propionibacterium acnes protein. The invention also relates to
polypeptides encoded by the polymuclectides (ARM35524-ARM64556) and to
immunogenic fragments of P. acnes polypeptides. The invention
additionally encompasses expression vectors and host cells comprising a
continuously encompasses expression vectors and host cells comprising a
compression proteins comprising a polypeptide of the invention, a
method for stimulating an immune response specific for a P. acnes
compression isolated T cell population comprising P acnes polypeptides,
distributed and an isolated T cell population comprising P. acnes polypeptides,
distributed and an isolated and an isolated T cell populations, or
polypeptide and an isolated spression (comprising P. acnes polypeptides,
distributed and an expression proteins, T cell populations, or
polymuclectides, antibodies, fusion proteins, T cell populations, or
conferentian and amethod for inhibiting the development of P. acnes in a
patient; and a method for inhibiting the development of P. acnes in a
patient; and a method for inhibiting the development of P. acnes in a
patient; and a method for inhibiting the development of P. acnes in a
patient; or for stimulations or antigen-presenting cells that express the
polymucleotides are useful for diagnosing, preventing or treating acne
vulgaris, or for stimulating an immune response specific for a P. acnes
confunction of an immune response against P. acnes, or for treating acne,
and the kit is useful for performing a diagnostic assay The present
confunction of an immune response against P. acnes, or for treating acne,
and the kit is useful for performing a diagnostic assay The present
conford by an ORP (open reading frame) contained within the P.
canes polymucleotides of the invention. Note: The sequence data for this
petent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at
cons polymucleotides.

Sequence 258 AA;

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3
                                                                                                                                          55 SGOILVEDVDLLKLSTRKORLYRKNTVGYLFQDYALIPDRTVKFNLOLAVEKHKWPEIPQ 114
                                                                        54
                                                                                                       93
                                                                                                                                                            94 SGTVFVEGSDIYSLSTSERDDIRLNRIGMIFQEHSLIVDFTVRENVELILRVRGFGSRSR
                                                                       12 GVRILWQGLSHKF------LPGTMTALTGASGSGKSTLLNCLGTLDKPS
                                                                                                      34 GGSIVASGVSHNFSTTHNRNLVLDDVTVSMQPGVMTLLHGVSGSGKTTLLNIMSGLLKPT
                                      65; Indels 24; Gaps
; Score 359; DB 6; Length 258; 
; Pred. No. 9.9e-31; 
36; Mismatches 65; Indels 2
       35.2%;
                    l Similarity 40.59
85; Conservative
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115 V-----LHAVGLESFEEKPVFELSGGEQQRTALARVILKAVFRIILADEPTGALDLTNSEL 169

20 LSHKFLPGIMTALTGASGSGKSTLINCLGTLDKPSSGQILVEDVDLLKLSTRKQRLYRKN 79

8 8

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The invention relates to an isolated nucleic acid derived from Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 acquential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a crecombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 364 disclosed sequences encoding 364 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions resulting from E. faecium bacterial infection (e.g. urinary tract infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans nucleic acid is useful for recombinant production of Candida albicans and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ς,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                  Vaccine, urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.6%; Score 353; DB 7; Length 27 40.9%; Pred. No. 4.9e-30; tive 36; Mismatches 72; Indels
170 VIEALRALA--DKGATVVVATHSPLFRESA 197
                                    214 VFELLRALAEDEKGRIVVLSSHDPTAKEYA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 7219; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating Enterococcus faecium infections. one if the disclosed E. faecium proteins.
                                                                                                                                                                                                                                                   E. faecium protein sequence SEQ ID 7219.
                                                                                                                                   ADC97592 standard, protein; 270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0051571P.
98US-0085598P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00107532.
                                                                                                                                                                                                              01-JAN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                   Enterococcus faecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-799836/75.
N-PSDB; ADC93938.
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Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection.
                                                                                                                                                                            ADC97592;
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                                                                                                RESULT 13
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The invention relates to an isolated mucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that inhibits a biological pathway the gene product or that has an activity against a biological pathway to proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for redlular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent
TVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIP-QVLHAVGLESFEEKPVFELSGGEQQ 138
                      242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening
to
                                                                  RTALARVLLKNPRIILADEPTGALDLTNSELVIEALR-ALADKGATVVVATHSPLFRESA 197
                                                                                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                    Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                   encoded by Prokaryotic essential gene #21031.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 63428; 1766pp; English
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                                                                                                                                                                                                                                                  standard; protein; 466
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06-SEP-2001, 2001US-00948993.
25-OCT-2001, 2001US-0342923P.
08-FEB-2002, 2002US-00072851.
06-MAR-2002, 2002US-0362699P.
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Carr G
                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma genitalium.
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Trawick JD,
                                                                                                                                  DTIIKL 203
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DRVIHI 248
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                                                                                                                                                                                                                                                  ABU35504
                                                                                                                                                                                                                                                                                  ABU35504;
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Wall D,
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                                                                                                                                                                                                                  RESULT 14
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to which each of the strains is present in a culture or collection of brains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational for dury discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                137 QORTALARVLLKNPRIILADEPTGALDLTNSELVIEALRALADK-GATVVVATHSPLFRE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                             21 SHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSGQILVEDVDLLKLSTRKQRLYRKNT
                                                                                                                                                                                                                                                                                                                                                                             VGYLFQDYALIPDRTVKFNLQLAVEKHKWP----BIPQVLHAVGLESFEEKPVFELSGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΰ
                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                             34.6%; Score 353; DB 6; Length 466; 39.2%; Pred. No. 1.1e-29; tive 42; Mismatches 61; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Masignani V, Margarit Y RosI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus polypeptide SEQ ID NO 1354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP26089 standard; protein; 237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-2001; 2001WO-GB004789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                         Best Local Similarity 39.2
Matches 73, Conservative
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INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 SADTII 201
                                                                                                                                                                                                                Seguence 466 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436 LADLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40200234771-A2.
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Tettelin H;
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(GENO-)
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the sproteins have antibacterial and antiinflammatory activity. (I), mucleic acids encoding (I), ABN6604-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by C Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a compound binds to composition comprising (I) or a nucleic acid encoding (I), may be composition comprising (I) or a nucleic acid encoding (I), may be cused as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be cused in gene therapp. Abribodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
detecting a compound that binds to the protein
                                                    Claim 1; Page 3291; 4525pp; English.
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Sequence 237 AA;

58 ILVEDVDLLKLSTRKQRLYRKMTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIP-QVL 116 117 HAVGLESFEEKPVFELSGGEQQRTALARVILKNPRIILADEPIGALDLTNSELVIEALRA 176 2 IBINDLKKSF--GVRILWQG--LSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQ 34.5%; Score 352; DB 5; Length 237; 38.3%; Pred. No. 5.2e-30; Live 45; Mismatches 76; Indels 177 LAD-KGATVVVATHSPLFRESADTII 201 Query Match
Best Local Similarity 38.33
Matches 79; Conservative a q 임 ઠે ò δ

Search completed: July 27, 2004, 16:35:05 Job time : 56 secs

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Sequence 7219, Ap Sequence 2536, A Sequence 2536, A Sequence 12101, A Sequence 3925, Ap Sequence 5411, Ap Sequence 511, App Sequence 2931, Ap Sequence 213021, A Sequence 6517, Ap Sequence 6517, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5335, Ap Sequence 5335, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Ap Sequence 23361, Appli
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1019
1 MIEINDLKKSFGVRILWQGL.......vvvATHSPLFRESADTIIKL 203
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-107-532A-7219

US-09-134-001C-4600

US-09-134-001C-4600

US-09-134-000C-3925

US-09-134-000C-3925

US-09-134-000C-6157

US-09-134-000C-6167

US-09-134-000C-6167

US-09-134-000C-617

US-09-134-000C-617

US-09-134-001C-4595

US-09-134-001C-4595

US-09-134-001C-4595

US-09-134-001C-4595

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Maximum Match 100%
Listing first 45 summaries
                                                                    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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No.
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) NAME/KEY: misc_feature) LOCATION: (B) LOCATION 1...270) SEQUENCE DESCRIPTION: SEQ ID NO: 7219: US-09-107-532A-7219

292 28.7 350 4 US-09-107-532A-6978 Sequence 6978, Ap 292 28.7 360 4 US-09-543-691A-6466 Sequence 666, Ap 291 288.5 28.3 215 4 US-09-305-9084-64 Sequence 610973, A 281 288.5 28.3 215 4 US-09-305-9084-64 Sequence 610973, A 281 288.5 28.3 215 4 US-09-305-9084-64 Sequence 610973, A 281 288.5 28.3 215 4 US-09-305-9084-64 Sequence 610973, A 281 288.5 28.3 215 4 US-09-31A-20657 Sequence 20657, A 281 28.3 215 4 US-09-31A-20657 Sequence 6078, Appl 287.5 28.2 267 4 US-09-31A-01C-3731 Sequence 7731, Ap 287.5 28.2 266 4 US-09-107-523A-526 Sequence 7371, Ap 287.5 28.2 267 4 US-09-305-984-18 Sequence 18, Appl 284.5 27.9 215 4 US-09-305-984-18 Sequence 18, Appl 284.5 27.9 215 4 US-09-107-523A-2444 Sequence 18, Appl 284.5 27.9 215 4 US-09-107-523A-4444 Sequence 18, Appl 283.2 27.8 224 4 US-09-107-532A-4444 Sequence 14256, Appl 283.2 27.7 224 4 US-09-305-984-72 Sequence 72, Appl 283.2 27.7 224 4 US-09-305-984-74 Sequence 74, Appl 282.2 27.7 224 4 US-09-305-984-74 Sequence 74, Appl 282.2 27.7 224 4 US-09-305-984-74 Sequence 74, Appl	ALIGNMENTS	32A-7219 7219, Application US/09107532A 6583275 INFORMATION:	ANT: Lynn A Doucet OF INVENTION: NUCL ENTE	ERAPEUTICS CORPORATI	husetts	COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER CD/ROM ISO9660	OPERATING SYSTEM: «Unknown» OPERATING SYSTEM: «Unknown» OPERATING SYSTEM: «Unknown»	CONTAIN AFFICATION VALA: APPLICATION NUMBER: US/09/107,532A FILING DATE: APPLICATION DATE:	5,5	1/57	NAMA: AIINELLO, FAMELA DENEKE REGISTRATION NUMBER: 40,489 REFERENCE/DOCKET NUMBER: GTC-012	TELECOMMULICATION INFORMATION: TELEPHONE: (781)893-5007 TELEFAX: (781)893-8277	SEQ 1	TYPE: amino acia TOPOLOGY: linear MOLECULE TYPE: protein	αΣ	FEATURE:
დდდ დოთთი თ		RESULT 1 US-09-107-53 ; Sequence 7 ; Patent No.; GENERAL	APE	NO.		CON	£			; ; ATT		79.7	SEQ	MOL	ORI	

17;

Length 1049;

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396 LİBLRDIRKRYĞGNGTPEVEVL-KĞVSLSIHAĞEFVAIVGASĞĞĞKSTLMNILĞCLDRPS 454
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                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                    Query Match
32.4%; Score 330.5; DB 4
Best Local Similarity 37.3%; Pred. No. 7.9e-29;
Matches 81; Conservative 38; Mismatches 81
FILE REFERENCE: 107196.136
CURRENT APPLICATION WUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION WUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25336
LENGTH: 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12101, Application US/09489039A
Patent No. 6610836
                                                                                                                                                                                                    Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-12101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.3%;
35.0%;
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Best Local Similarity 35.0%
Matches 75; Conservative
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                                                                                                                                                                                                          ; ORGANISM: FSEUGO
US-09-252-991A-25336
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                                                                                                                                                                                   TYPE: PRT
ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn Dougette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT APPLICATION NUMBER: US 60/064,964 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR PLING DATE: 1997-11-08 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674 SEQ ID NOS: 5674
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MIBINDLKKSFGVRILWQGL---SHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQ
                                                                                             LSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILVEDVDLLKLSTRKQRLYRKN
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                        Length 270;
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                                                             72; Indels
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                        Query Match
34.6%; Score 353; DB 4;
Best Local Similarity 40.9%; Pred. No. 2.6e-32;
Matches 76; Conservative 36; Mismatches 72
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AM
TITLE OF INVENTION: ABRUGINOSA FOR DIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4600, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
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US-09-134-001C-4600
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US-09-252-991A-25336
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GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709-2004001

CURRENT PEPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 12101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 GTYRVAGTDIAQLDGDALARLREHFGFIFQRYHLLSHLTAAQNVEVPAVYAGNERRARL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 PEIPQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSEL 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 329; DB 4; Length 672;
; Pred. No. 6e-29;
44; Mismatches 83; Indels
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; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6167
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                                                                            Sequence 3925, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUMBER: US/09/134,000C
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1998-08-15
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 3925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 ILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNL------QLAVEXHK 108
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Patent No. 6342385

GENERAL INFORMATION:
TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
PILE REPERENCE: UAB-17402/22

CURRENT APPLICATION WUMBER: US/09/627,376

CURRENT FILING DATE: 2001-05-30

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.0

SEQ ID NO 15

LENGTH: 246

TYPE: PRT

ORGANISM: Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 31.6%; Score 322.5; DB 4; Length 246; Best Local Similarity 35.8%; Pred. No. 7.4e-29; Matches 78; Conservative 41; Mismatches 74; Indels 25
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209 VMAILHQLKAQGHTVIIVTHDPQVAAQAERIVEI
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; ORGANISM: Enterococcus faecalis
US-09-134-000C-3925
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US-09-627-376-15
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Sequence 541, Application US/09543681A

| Sequence 541, Application US/09543681A
| Patent No. 665709
| GENERAL INFORMATION:
| APPLICANT: GREY BRETON
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI)
| TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
| TITLE REPRENCE: 2709-1002-001
| CURRENT FILING DATE: 2000-04-05
| PRIOR FILING DATE: 2000-04-05
| PRIOR FILING DATE: 1999-04-09
| NUMBER OF SEQ ID NOS: 8344
| SEQ ID NO 5411 Second of the state of the stat 57 QILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQL-----AVEKHKW 109 ; | ; ; ; ; | ; | | | | ; | ; | | ; | | ; | | ; | ; ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; 10 PEIPQVLHAVGL-ESFEEKPVFELSGGEQQRTALARVLLKNPRIJLADEPTGALDLTNSE 168 61 SSCHIIFNNYQLEKVKDEEAAVFRSRHIGFIFQNFNLLNIFNNKDNLLIPVIISGSKVNS 120 .05 -EKHKWPEIPQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKOPRIILADEPTGALD 1 MIBINDLKKSF----GVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSG Query Match 31.5%; Score 321; DB 4; Length 653; Best Local Similarity 35.8%; Pred. No. 4.8e-28; Matches 77; Conservative 46; Mismatches 78; Indels 1 164 LINSELVIEALRALADKGATVVVATHSPLFRESADTII 201 169 LVIEALRALADKGATVVVATHSPLFRESADTIIKL 203 TYPE: PRT ORGANISM: Proteus mirabilis RESULT 7 US-09-543-681A-5411 RESULT 8 US-09-134-000C-6167 ÚS-09-543-681A-5411 LENGTH:

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62 DVDLLKLSTRKQRLYR-----KNTVGYLFQDYALIPDRTVKFNL-----QLAVEK 106
                                                                                                                                                                                                                                                                                                                                  98 Q-ETLKLKSHKGELVAADNKQLEKLRSKIGFVFQNFNLWFHKTILQNIIEGFTQVLGISK 156
                                                                                                                                                                                                                                                                                                                                                                                     107 -HKWPEIPQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLT 165
                                                                                                                                                                                                                                                                                                                                                                                                             38 LDLQDIHKSYGSLEVLKGVSLTAYDGDVISILGSSGSGKSTLLRCINLLEKPTSGKIIVG 97
                                                                                                                                                                                                                                 2 IEINDLKKSFGVRILMQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILVE
                                                                                                                                                         Length 286;
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 NSELVIEALRALADKGATVVVATHSPLF-RESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 LVNEVLAVMRELADEGRIMLIVTHEMRFAREVSSKVVFL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 30.1%; Score 306.5; DB 4; Best Local Similarity 36.5%; Pred. No. 6.2e-27; Matches 76; Conservative 40; Mismatches 83;
                                                                                                                                                           30.2%; Score 308; DB 4; llarity 34.2%; Pred. No. 4.4e-27; Conservative 50; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RALADKGATVVVATHSPLF-RESADTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-09-134-001C-3832
; Sequence 3832, Application US/09134001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13021
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2931
LENGTH: 286
                                                                                                    ORGANISM: M.catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                           Best Local Similarity
Matches 75; Conserv
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US-09-489-039A-13021
                                                                                                          ; OKGANISH: M.CA
US-09-540-236-2931
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Sequence 2931, Application US/09540236
Datent No. 6673910
GENERAL INFORMATION: Distance to al.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 2709,2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCRMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTENCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 5879
                                                                                                                                                                                                                                                          133 XAIAE--KYLKIVGLETKAKSKVTELSGGQQQRVAIARSLVNDPLLIMADEPTGALDSET 190
                                                                                                                                                           GQILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQL------AVEK 106
                                                                                                                                                                                                                                     107 HKWPEIPQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 DYALIPDRIVKFNLQLAV-----EKHKWPEIPQVLHAVGLESFEEKPVFELSGGEQORT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 ALARVLLKNPRIILADEPIGALDLINSELVIEALRALADKGATVVVATHSPLFRESADTI 200
                                                                                                          14 LIBLADINKFYPVGKEKLHVL-KELNLTIHQGEFILIMGKSGSGKTTLMNIIGFLDRLTD 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 GTMTALTGASGSGKSTLLNCLGTLDKPSSGQILVEDVDLLKLSTRKQRLYRKNTVGYLFQ 86
                                                                                1 MIEINDLKKSFGV-----RILWQGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSS
                                                                                                                                                                                   GSYHFSGTDVSKLSENKKSAFRNEYLGFIFOOFFLINSLNVSQNVQLPCVYEGKKSRAEK
                                              Gaps
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                                            17;
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        Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.9%; Score 315; DB 4; Length 226; 38.3%; Pred. No. 4.8e-28; Live 36; Mismatches 71; Indels
                                            Indels
                                                                                                                                                                                                                                                                                                                                  GTEIMELLKELNEGGKTIVWVTHDEDMKKYASRVIHM 227
                                                                                                                                                                                                                                                                                                                SELVIEALRALADKGATVVVATHSPLFRESADTIIKL 203
        DB 4;
                                              81;
        ; Score 320.5; DB 4; Pred. No. 1.2e-28; 41; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5879, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Enterococcus faecalis
US-09-134-000C-5879
        31.5%;
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Best Local Similarity 38.3%,
T0; Conservative
                                            Conservative
                          Similarity
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        Query Match
Best Local Simi
Matches 78;
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Sequence 13021, Application US/09489039A
Sequence 13021, Application US/09489039A
Sequence 13021, Application US/09489039A
Sequence 13021, Application US/09489039A
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE PERRINCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 VLHAVGLESFEEKPVFELSGGEQORTALARVLLKNPRIILADEPIGALDLINSELVIEAL 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 IEINDLKKSFGVRILMOGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILVE
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Sequence 6517, Application US/09134000C
EREAL INFORMATION:
APPLICANT: Lynn boucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT PAPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 ILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQVLH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 ILFKNED---IQNKGYSNHRKANISLVFQNYNLIDYLSPIENIRLVNKSAD----ESILF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 AVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEALRA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 ELGLDKKOIKRNVWKLSGGOORVAIARALVSDAPIILADEPIGNLDSVTAGEIINILKT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 ILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQVLH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 İLFKNED---IQNKGYSNHRKANNISLVFQNYNLIDYLSPIENIRLVNKSAD----ESILF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .18 AVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEALRA 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MIEINDLKKSFG---VRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.0%; Score 305.5; DB 4; Best Local Similarity 37.5%; Pred. No. 5.8e-27; Matches 78; Conservative 45; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
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1 Similarity 37.5%; Pred. No. 5.8e-27;
78; Conservative 45; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...221
SEQUENCE DESCRIPTION: SEQ ID NO: 6667:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || |: |:| || | :|
178 LAKDRNKCVIVVTHSKEVADSADIILEL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LA-DKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
PELECOMMUNICATION INFORMATION
                              TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6667:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-107-532A-6667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-134-000C-6517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
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                 GENERAL INCREMENTATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: WICKLET ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEIDERNIDIS PRO DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT PILING DATE: 1998-08-13
PRIOR PELING DATE: 1997-08-14
PRIOR PILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6667, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Acid AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQVLHAVG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- ELSGGEOORTALARVLLKNPRIILADEPTGALDL 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 30.0%; Score 306; DB 4; Length 242;
Best Local Similarity 33.5%; Pred. No. 5.8e-27;
Matches 73; Conservative 44; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:::| ||:: | EVVGDVLKVMRQLANESMTWVIVTHEMNFAKEISDKVV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 TNSELVIEALRALADKGATVVVATHSPLF-RESADTII 201
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APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LESFEEKPVF-------
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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RESULT 15
US-09-489-039A-10491
iS-09-489-039A-10491
j Sequence 1041, Application US/09489039A
j Sequence 1041, Application US/09489039A
j Sequence 1041, Application US/09489039A
j Patent No. 6610836
j GENERAL INFORMATION:
i TITLE OF INVENTION:
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Query Match
Best Local Similarity 35.3%; Pred. No. 2.7e-26;
Matches 73; Conservative 45; Mismatches 73; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | | :: | | | | :: | 1.0 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.
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61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPE-----IPQ 114

1 MIEINDLKKSFGVRILMQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60

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115 VLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALD-LTNSELVIEA 173

174 LRALADKGATVVVATHSPLFRESADTI 200

Search completed: July 27, 2004, 16:37:19 Job time : 24 secs

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July 27, 2004, 16:36:31; Search time 45 Seconds (without alignments) 1412.673 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1288442
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1288442 seqs, 313154207 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1019
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

·	Description	Sequence 389, App	Sequence 386, App	Sequence 11171, A	Sequence 64080, A	Sequence 63428, A	Sequence 67001, A	Sequence 4456, Ap	squence 442, App	Sequence 13995, A	Sequence 44079, A	Sequence 12964, A	Sequence 13482, A	nence 5642, Ap	Sequence 12706, A	Sequence 1256, Ap
	Desc	Š	တိ	യ്	Š	ഗ്ഗ	Š	Sec	တိ	Sec	Š	Š	Sec	Sec	Sec	S
SUMMARIES	OI	US-10-474-776-389	US-10-474-776-386	US-10-156-761-11171	US-10-282-122A-64080	US-10-282-122A-63428	US-10-282-122A-67001	US-09-738-626-4456	US-10-627-476-442	US-09-815-242-13995	US-10-282-122A-44079	US-10-156-761-12964	US-09-815-242-13482	US-09-815-242-5642	US-09-815-242-12706	US-10-238-075-1256
	DB	16	16	14	12	12	12	σ	12	σ	12	14	σ	σ	σ	14
	Match Length DB	213	210	248	465	466	227	222	222	648	252	315	236	249	252	231
* Query	Match	39.2	37.3	36.5	35.6	34.6	33.8	33.3	33.3	33.3	33.1	33.0	33.0	33.0	33.0	32.7
	Score	399	380.5	371.5	362.5	353	344.5	339.5	339.5	339	337	336.5	336	336	336	333.5
Result	No.	н	7	m	4	5	9	7	80	D	10	11	12	13	14	15

70852, 11869, A 20, App 60354,	Sequence 62554, A Sequence 64477, A Sequence 14933, A Sequence 71920, A Sequence 10091, A Sequence 13827, A	Sequence 53217, A Sequence 10577, A Sequence 61025, A Sequence 15, Appl Sequence 1350, A	51556 70384 56935 46313 51603 11088	Sequence 6814, Ap Sequence 334, App Sequence 52619, A Sequence 64068, A Sequence 69667, A Sequence 10135, A Sequence 5304, Ap
US-10-282 US-09-815- US-10-246 US-10-282		12 US-10-282-12A-5217 US-09-815-242-10577 12 US-10-282-122A-61025 13 US-10-047-66A-15 9 US-09-815-242-13350 9 US-09-815-242-13690	0-282-12 0-282-12 0-282-12 0-282-12 0-282-12 0-282-12	9 US-09-738-626-6814 12 US-10-627-476-334 12 US-10-627-476-334 12 US-10-282-122A-5619 12 US-10-282-122A-59667 9 US-09-815-242-10135 9 US-09-738-626-6304
252 663 241	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2548 2546 271 271	256 244 244 244 243 262 262 262	0022222 002222 002222
6 4 4 4 6		31.8 31.8 31.5 31.5 5.5	31.5 30.8 30.8 30.7 30.7	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
330.5 330.5 330.5	3329 322 323 323 325 335 355 355 355 355 355	323 323 323 323 323 321 321	320.5 315 314 314 312.5 312.5	3111 310.5 310.5 310 310 309.5
11 11 11 11 11 11 11 11	222 2 2 2 2 2 2 2 2 3 2 3 2 3 3 3 3 3 3			60 11 12 16 14 15 15 15 15 15 15 15 15 15 15 15 15 15

ALIGNMENTS

KESULT 1 US-10-474-776-389 ; Sequence 389, A ; Publication No. ; GENERAL INFORMA	SULT 1 -10-474-776-389 Sequence 389, Application US/10474776 Publication No. US2040110181A1 ApplicANT Winch Winch Will Sequence 3
TITLE (TITLE (FILE RE CURRENT	ON: NO AMIOO
CURRENT FILL CURBER OF SE SOFTWARE: Pa SEQ ID NO 389	CORRENT FLING DATE: 2003-10-14 NUMBER OF SEQ ID NOS: 752 SOFTWARE: Patentin version 3.1 EQ ID NO 389
; TYPE: PRT ; ORGANISM: Str US-10-474-776-389	TYPE: PRT ORGANISM: Streptococcus pneumoniae 0-474-776-389
Query Match Best Local Matches 9	tch 39.2%; Score 399; DB 16; Length 213; al Similarity 42.9%; Pred. No. 3.3e-34; 90; Conservative 40; Mismatches 70; Indels 10; Gaps 3;
δ,	1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60
QQ	
λ̈́O	61 BDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVBKHKWPEIFQVLHAVG 120
Db	61 GGKDLKTIPTREYFRDQMGYLFQNFGLLENGSIKENLDLGFVGQKISKVERLERQVG 117
δ	121 -LESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
Db	118 ALEKVNLGYLDLEÇKIYTLSGGEAQRVALAKTILKNPPLILADEPTAALDPENSEEVMNL 177
ò	174 LRALADKGATVVVATHSPLFRESADTIIKL 203
Dp	178 LVDLKDENRIIIIATHNPLVWNKADEIIDM 207

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APPLICANT: Kamamoco, Kodert
APPLICANT: Kamamoco, Kodert
APPLICANT: Ku, H.
APPLICANT: Ku, H.
APPLICANT: Ku, H.
APPLICANT: Ku, H.
APPLICANT: Ku, H.
APPLICANT: Ku, H.
APPLICANT: Ku, H.
APPLICATION INDER: US/10/282,122A
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/203,335
PRIOR APPLICATION NUMBER: 60/203,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/243,625
PRIOR APPLICATION NUMBER: 60/243,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/263,636
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
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PRIOR PILING DATE: 2000-11-22
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PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
                                                                                                                                                  113 PQVLHAVGLESFEEKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIE 172
                                                                                                                                                                                                                                                               57 QILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFN----LQLAVEKHKWPEI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MIEINDLKK--SFGV--RILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSG 56
                                    2 IEINDLKKSFG-----VRILMQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSG
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SOFTWARE: PatentIn version 3.1
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35.6%; Score 362.5; DB 12; Length 465;
Best Local Similarity 36.7%; Pred. No. 8.1e-30;
Matches 77; Conservative 54; Mismatches 70; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                             188 LLRGMVDSEGQTVIMVTHDFVAASYADRVVFL 219
                                                                                                                                                                                                                                                                                                                                              173 ALRALAD-KGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 64080, Application US/10282122A
Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Maselbeck, Robert
APPLICANT: Oblese, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto, Robert
Forsyth, R.
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Wall, Daniel
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Carr, Grant
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LENGTH: 465
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                                                                                                 Sequence 386, Application US/10474776
Sequence 386, Application US/10474776
Subjication No. US20040110181A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYF
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
FILE REFERENCE: AM100649-PCT
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT APPLICATION NUMBER: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEI-----PQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 RGKD---LANYKSSDFPRHELGYLFQNFGLIENQSIEENLKLGLIGQKLSRSEQRLRQKQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MIELKQVSKSFGERELFSNLSMTFEAGKVYALIGSSGSGKTTLMMMIGKLE-PYDGTIFY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 37.3%; Score 380.5; DB 16; Length 210; Best Local Similarity 41.0%; Pred. No. 3.1e-32; Matches 86; Conservative 41; Mismatches 72; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 LRALADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ISHLKAWA, JUNA
APPLICANT: ISHLKAWA, HINGOSHI
APPLICANT: HOSIKAWA, HINGOSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US,10/156,761
CURRENT FILLING DATE: 2002-05-29
PRIOR PILLING DATE: 2001-05-30
PRIOR PILLING DATE: 2001-05-30
PRIOR PILLING DATE: 2001-05-30
PRIOR PILLING DATE: 2001-05-30
PRIOR FILLING DATE: 2001-08-02
NUMBER OF SEO ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-156-761-11171
; Sequence 11171, Application US/10156761
; Publication No. US/20030119018A1
; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Streptococcus pneumoniae US-10-474-776-386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRGANISM: Streptomyces avermitilis US-10-156-761-11171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 11171
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEO ID NO 386
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Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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APPLICANT: Carr, Grant
APPLICANT: Vanamoto, Robert
APPLICANT: Vanamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR PELING DATE: 2000-03-02-20
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
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PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-22
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/26,636
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/26,636
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-09
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PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
                                                                                                                                        137 OORTALARVLIKNPRIILADEPIGALDLINSELVIEALRALADK-GATVVVATHSPLFRE 195
                                                                                                                                                                                  VGYLFQDYALIPDRTVKFNLQLAVEKHKWP----EIPQVLHAVGLESFEEKPVFELSGGE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MIBINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV
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1 Similarity 40.1%; Pred. No. 2.5e-28;
83; Conservative 34; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 67001, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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ORGANISM: Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang, Liangsu
Zamudio, Carlos
Andone, Cheryl
Haselbeck, Robert
Ohleen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamanoto, Robert
Forsyth, R.
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436 LADLVI 441
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Best Local Similarity
Matches 83; Conserv
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APPLICANT: Carry Grant
APPLICANT: Carry Carry
APPLICANT: APPLICANT: Carry
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
ITILE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/2030,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
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PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/267,636
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION N
                                                                                                                     113 POVLHAVGLESFEEKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIE 172
                                                                                                                                                                                                                                                          231 IIELKNVYKYITNGVTTNAVLKGIDLKLKAHDFIVILGPSGSGKTTLLNIISGMDRPSSG 290
                                                                        57 QILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPE----1 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels '10;
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34.6%; Score 353; DB 12; Length 466;
Best Local Similarity 39.2%; Pred. No. 8.5e-29;
Matches 73; Conservative 42; Mismatches 61; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                           |: | |: | : | |: | 410 PELAIKQRYKTTMVIVTHNNLIAQLADLVI 440
                                                                                                                                                                                                                                                                                                                                                                 173 ALRALADK-GATVVVATHSPLFRESADTII 201
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US-10-289-122A-63428
Sequence 63428, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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ORGANISM: Mycoplasma genitalium
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APPLICANT: Zamudio, Carlos
APPLICANT: Haelbeck, Robert
APPLICANT: Haelbeck, Robert
APPLICANT: Oblisen, Rari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Trawick,
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APPLICANT: Trawick, John D. APPLICANT: Carr, Grant J. APPLICANT: Yamamoto, Robert T.
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Best Local Similarity
Matches 80; Conserv
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ORGANISM:
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                                                              121 QVGLAHRFDHRP-SQLSGGEQQRVCIARALVNQPPVIFADEPIGNLDEKNEQLVLDLLVT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 QILVEDVDLIKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVE---KHKWPEIP 113
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                                       118 AVGL-ESFEEKPVFELSGGEQQRTALARŲLLKNPRIILADEPTGALDLTNSELVIEALRA 176
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38.1%; Pred. No. 8.3e-28;
tive 38; Mismatches 83;
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                                                                                                                                                                                                                                                                                                                      APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGURII, HIROSHI
APPLICANT: MIZOGURII, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: OCCHIAL, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TANEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILICA DATE: 2000-12-18
                                                                                                                                                 177 LADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                           Sequence 4456, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 442, Application US/10627476
Publication No. US20040030116A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pompejus, Mark
APPLICANT: Kroger, Burkhard
APPLICANT: Schoder, Hartwig
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Best Local Similarity
Matches 80; Conserv
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LENGTH: 222
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APPLICANY: ACCOUNT GREEN CORYNEAGURE TITLE OF INVENTION: CORYNEAGURENT GREEN CONTINGATION: TITLE OF INVENTION: CORYNEAGURENT GREEN CONTINGATION: TITLE OF INVENTION: INVOICED IN MEMBRANE SYNTHESIS AND MEMBRANE TITLE OF INVENTION: TRANSPORT TITLE OF INVENTION: TRANSPORT CONTINGATION: TRANSPORT TITLE REFERENCE: BG1-125CPCN
FILE REFERENCE: BG1-125CPCN
CURRENT APPLICATION NUMBER: US/0602,787
PRIOR PILLING DATE: 1090-06-23
PRIOR FILLING DATE: 1990-06-25
PRIOR FILLING DATE: 1990-06-25
PRIOR FILLING DATE: 1990-06-25
PRIOR PILLING DATE: 1990-07-08
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Proharyotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83;
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ilarity 38.1%; Pred. No. 8.3e-28;
Conservative 38; Mismatches 83
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskird, Judith W.
APPLICANT: Trawick, John D.
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63 VIANGQELNKLNQKALAKFRKESLGFIFQDYSILPTLTVKENIMLPLSVQKMSKATMEEN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 ILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQ--- 114
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    PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
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Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: ISHIKAWA, JUN

APPLICANT: ISHIKAWA, JUN

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: HATTORI, MASHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT APPLICATION NUMBER: US/201-204089

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR PELICATION NUMBER: JP 2001-204089

PRIOR PELICATION NUMBER: JP 2001-272697

PRIOR PLING DATE: 2001-05-30

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 12964
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; ORGANISM: Streptomyces avermitilis
US-10-156-761-12964
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.0348
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/203,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MIEINDLKKSF-----GVRILWQGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
33.3%; Score 339; DB 9; Length 648;
Best Local Similarity 36.9%; Pred. No. 4.3e-27;
Matches 79; Conservative 42; Mismatches 81; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 VIBALRALADKGATVVVATHSPLFRESADTIIKL 203
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CURRENT FILING DATE: 2001-03-21
PRIOR PLILING DATE: 2001-03-21
PRIOR PLILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-110-23
PRIOR PLILING DATE: 2000-110-27
PRIOR PLILING DATE: 2000-110-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-12-27
PRIOR PLILING DATE: 2000-12-27
PRIOR PLILING DATE: 2000-12-26
PRIOR FILING DATE: 2001-12-26
PRIOR PLILING DATE: 2010-10-216
NUMBER OF SEQ ID NOS: 14110
SOPTWARE: PASISEQ for Windows Version 4.0
SOD ID NO 13995
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Sequence 44079, Application US/10282122A
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Yall, Daniel
APPLICANT: Yall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoro, Robert
APPLICANT: Yamamoro, Robert
APPLICANT: Yamamoro, Robert
APPLICANT: Yamamoro, Robert
APPLICANT: Yamamoro, Robert
APPLICANT: Yamamoro, Robert
APPLICANT: Yamamoro, Robert
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ORGANISM: Salmonella typhi
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US-10-282-122A-44079
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Gaps

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4
                                                       Gaps
                                                       11;
Query Match 33.0%; Score 336.5; DB 14; Length 315; Best Local Similarity 37.7%; Pred. No. 2.8e-27; Matches 80; Conservative 39; Mismatches 82; Indels 11;
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Sequence 12706, Application US/09815242 Patent No. US2020061569A1 NPDERAL INFORMATION: APPLICANT: Haselbeck, Robert
199 TIIKL 203
                                                                  210 RVIQM 214
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US-09-815-242-12706
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SEQ ID NO 5642
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                                                                                                                                                      57 QILVEDVDLLKLSTRKQRLYRKOTVGYLFQDYALIPDRTVKFN----LQLAVEKHKWPEI 112
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2 IEINDLKKSFG----VRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSG 56
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Best Local Similarity 40.5%; Pred. No. 2.1e-27;
Matches 75; Conservative 38; Mismatches 58; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Drokaryotes
FILE REFERENCE: ELITRA.011A
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 ALRALAD-KGATVVVATHSPLFRESADTIIKL 203
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SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ 10 13482
LENGTH: 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-12-22
PRIOR PRILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick John D.
Carr, Grant J.
Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 ILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIFDRTVKFNLQLAVEKHKMPEIPQ--- 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MIEINDLKKSFGVRILWOGL --- SHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSGQ 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
33.0%; Score 336; DB 9; Length 249;
Best Local Similarity 34.7%; Pred. No. 2.3e-27;
Matches 74; Conservative 47; Mismatches 82; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 BALRALADK-GATWWATHSPLFRESADTIKL 203
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILLING DATE: 2000-03-21
PRIOR PELLON INVIBER: 60/206,848
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR FILLING DATE: 2000-05-23
PRIOR FILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-12-27
PRIOR PELLING DATE: 2000-12-27
PRIOR PELLING DATE: 2000-12-27
PRIOR PELLING DATE: 2001-22-2
Sequence 5642, Application US/09815242
Patent No. US20020051569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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US-09-815-242-5642
                                                                                                                                                  Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                              Ohlsen, Kari L.
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71 GTDAAALDEEGRRRFRAEKIGLVFQQFHLIPFLTALENIMLAQHYHSVVDEAAARKVLEQ 130
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                                                                                                                                                                                                                                                            2 IEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILVE 61
                                                                                                                                                                        Gaps
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                                                                                                            Length 231;
                                                                                                         Query Match
32.7%; Score 333.5; DB 14; Length
Best Local Similarity 38.0%; Pred. No. 3.8e-27;
Matches 78; Conservative 32; Mismatches 92; Indels
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                           , ORGANISM: Bscherichia coli
US-10-238-075-1256
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APPLICANT: Ohlsen, Kari I.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Travial, John D.
APPLICANT: Travial, John D.
APPLICANT: Travial, John D.
APPLICANT: Travial, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
ITILE OF INVENTION: Identification of Essential Genes in
TILLE OF INVENTION: Identification of Essential Genes in
TILLE OF INVENTION: Identification of Essential
FILE REPERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/205,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,938
PRIOR APPLICATION NUMBER: 60/253,938
PRIOR APPLICATION NUMBER: 60/253,938
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-26
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2001-02-16
NUMBER OF ESQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12706
LENGTH: 252
TWOND: DRAFF
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33.0%; Score 336; DB 9; Length 252;
Best Local Similarity 34.7%; Pred. No. 2.3e-27;
Matches 74; Conservative 47; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12706
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Sequence 1256, Application US/10238075
Publication No. US20030148324A1
Publication No. US20030148324A1
APPLICATION NO. US20030148324A1
APPLICATION I.N.S.E.R.M.
TITLE OF INVENTION: E.coli, and biological uses of these polynuclectides and of their TITLE OF INVENTION: E.coli, and biological uses of these polynuclectides and of their FILE REFERENCE: BLANDINE
CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR FILING DATE: 2000-01-10
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: Patentin version 3.1
SEQ ID NO 1256
ILBNGTH: 231
TYPE: PRI

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172 EALRALADK-GATVVVATHSPLFRESADTIIKL 203

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US-10-238-075-1256

1 MIEINDLKKSFGVRILWQGL---SHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQ

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- protein search, using sw model OM protein July 27, 2004, 16:33:10 ; Search time 16 Seconds (without alignments) 1220.430 Million cell updates/sec Run on:

US-09-868-338-9 1019 1 MIEINDLKKSFGVRLLWQGL......VVVATHSPLFRESADTIIKL 203 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	1 1	ABC transporter, A	hypothetical prote	ABC transporter, A	ä	thetical prot		ter,	thetical prot	ter (ransport	glutamine transpor	ABC transporter, A	transporter A			transporter (41	ranspc	ABC Transporter UU			probable ABC trans	ransport	tran	sporter,	thetical prot	l prot	ter	rter A
	QI		ກ	979	52	980	950	D97884	52	980	A84088	B86626	34		AB3297	A83685	B69377	A84109	64	9708	A82932	9708	E90216	82	B69477	D81263	12	E90749	0	F96955	3482
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115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173

| :| : | :::|||:| | :| 174 LRALADKGATVVVATHSPLFRESADTIIKL 203

8 & 8 &

RESULT 2
B97947

Hypothetical protein ABC-NBD [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: B97947
R;Hoskins, J.A., Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Ese, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.; McY, P.; Sun, P.M.; Winkler, M.E.

ABC transporter, A	probable ABC trans	hypothetical prote	ABC transporter, A	ABC transporter, A	ABC transporter AT	conserved hypothet	ABC transporter, A	hypothetical prote	ABC transporter (A	ABC transporter, A	hypothetical prote	ABC transporter AT	ABC transporter, A	ABC transporter, A	ABC transporter, A
AC1796	F95337	T47012	AE0237	AI1580	F86843	AF0609	AH1167	D90079	A70074	H72342	H98058	G96929	AG1227	C95192	C97001
7	N	N	N	N	N	(7)	N	7	~	7	N	~	~	7	0
207	304	237	237	233	259	648	999	252	257	228	236	238	233	233	234
33.6	33.6	33.5	33.5	33.4	33.3	33.3	33.2	33.1	33.1	33.0	33.0	32.8	32.7	32.7	32.5
342	342	341.5	341.5	340	339	339	338.5	337	337	336	336	334.5	333	333	331
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4. S

ALIGNMENTS

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PIDN:AAK74298.1; PID:914971578; GSPDB:GN00164; TIGR:SP46
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                                                                                                                                                                                                                                                                                                                                                             R.H.; Jaskunas, S.R.;
                                                                                                                           hypotherical protein ABG-NBD [imported] - Streptococcus pneumoniae (strain R6) (Species: Streptococcus pneumoniae (Species: Streptococcus pneumoniae (Species: Streptococcus pneumoniae (Space: 22-0ct-2001 #sequence_revision 22-0ct-2001 #text_change 22-0ct-2001 C;Accession: G98096 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; S;Hoskins, J.A.; Alborn Jr., W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Iy, P.; Sun, P.M.; Winkler, M.E. Totol J. S.; J. Sun, P.M.; Winkler, M.E. J. 2001 J. J. Shatthors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R. A;Hitle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SP0111 (imported) - Streptococcus pneumoniae (strain TIGR4)
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A;Residues: 1-213 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAL00604.1; PID:g15459486; GSPDB:GN00174
C;Genetics: A;Genetics: A;Gene: ABC-NBD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LESFE-----EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
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; Pred. No. 3.6e-26;
45; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 399; DB 2; L
Pred. No. 2.6e-27;
40; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 LRALADKGATVVVATHSPLFRESADTIKL 203
178 LVDLKDENRIIIIATHNPLVWNKADEIIDM 207
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A,Cross-references: GB:AE005672; PII
A,Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.2%;
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Best Local Similarity 40.2%;
Matches 84; Conservative 49
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A;Status: preliminary
A;Molecule type: DNA
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A;Gene: SP0111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1987
                                    S. R.
         J. Bacteriol. 183, 5709-5717, 2001
A, Atthors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, thritle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Reference number: A97872; MuID:21429245; PMID:11544234
A; Accession: B97947
A; Returus: preliminary
A; Molecule type: DNA
A; Rederence number: A07872; MuID:2142945; PMID:11544234
A; Molecule type: DNA
A; Residues: 1-213 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LESFE-----EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
                                                                                                                                                                                                               A;Residues: 1-213 <KUR> '
A;Cross-references: GB:AE007317; PIDN:AAK99406.1; PID:g15458184; GSPDB:GN00174
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKWPEIPQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRILLADEPTGALDLTNSELVIEA 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MIELKNISKKFGSRQLFSDTNLHFEGGKIYALIGTSGCGKTTLLNMIGRLEPYDKGQIIY
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                                                                                                                                                                                                                                                                                                                                                                                                          69; Indels
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                                                                                                                                                                                                                                                                                                                                                    39.7%; Score 405; DB 2;
41.9%; Pred. No. 7.9e-28;
tive 43; Mismatches 69
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LESLKNPNRTIIIATHNPLIWEQVDQVIRV 207
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Best Local Similarity
Matches 88; Conserv
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Matches 90; Conserv
                                                                                                                                                                                                                                                                                                   A; Gene: ABC-NBD
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A/Cross-references: GB:AE005672; PIDN:AAK76024.1; PID:gl4973462; GSPDB:GN00164; TIGR:SP46
A/Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1957
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84088
ABC transporter (ATP-binding protein) BH3505 [imported] - Bacillus halodurans (strain C-1
C;Species: Bacillus halodurans
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J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Authors: Apple Bacterium Streptococcus pneumoniae Strain R6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV
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                                                                                                                                                                                                                                                                                                                            Query Match 37.3%; Score 380.5; DB 2; Best Local Similarity 41.0%; Pred. No. 1e-25; Matches 86; Conservative 41; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 380.5; DB 2;
; Pred. No. 1e-25;
41; Mismatches 72;
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LLSLRDDNRLIIIATHNPAIWEMADEVFTM 206
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Matches 86; Conservative
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A, Status: preliminary
A, Molecule type: DNA
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D97884
hypothetical protein ABC-NBD [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001
C;Accession: D97884
E; Abborn D77884
C;Accession: D97884
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ABC transporter, ATP-binding protein SP1957 [imported] - Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Dates: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: 03-5228
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Scatus: preliminary
A;Scatus: preliminary
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Best Local Similarity 39.7
Matches 83; Conservative
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ABC transporter, ATP-binding protein homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C;Accession: D69433
R;Kench, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, S; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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R;Athors: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A;Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                    Glutamine transport ATP-binding protein glnQ - Mycoplasma pneumoniae (strain ATCC 29342)
N.Alternate names: hypothetical protein R02_orf465
A.Species: Mycoplasma pneumoniae
A.Yariety: ATCC 29342
A.Yariety: ATCC 29342
C.Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 02-Feb-2001
C.Accession: 873400
R.Hihmmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
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A.Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.
A.Reference number: 87327; MUID:97105885; PMID:8948633
A.Accession: 87340
A.Accession: 87340
A.Residus: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Molecule type: DNA
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C,Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;23-219/Domain: ATP-binding cassette homology <ABC>
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     A; Molecule type: DNA
A; Residues: 1-226 < KLE>
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A;Genetic code: SGC3
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 17-May-2002
A;Accession: A84088
R;Takeni, H.; Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84088
A;Accession: A84098
A;Accession: Aperican and A;Residues: 1-228 <500
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BR6626

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BRC transporter ATP-binding protein yabE [imported] - Lactococcus lactis subsp. lactis
C; Species: Lactococcus lactis subsp. lactis
C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C; Accession: B86626

R; Bolotin, A.; Winoker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
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A; Ritler The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A; Reference number: A86625; MUID:21235186; PMID:11337471
A; Bolocule type: Dreiminary
A; Bolocule type: Dreiminary
A; Bolocule type: Dreiminary
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A;Experimental source: strain C-125
C;Genetics:
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C,Superfamily: short-chain ATP-binding cassette proteins, ATP-binding cassette homology
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A; Cross-references: GB:AE005176; PID:g12722846; PIDN:AAK04108.1; GSPDB:GN00146
A; Bxperimental source: strain IL1403
A; Genetics: A
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ABC transporter, ATP-binding protein homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
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C;Accession: B63377
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.Fisischmann, R.D.; Quackenbuch, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glock, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-228 kLDs
A;Cross-references: GB:AE001033; GB:AE000782; NID:g2689356; PIDN:AAB90224.1; PID:g2649576
C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology
C;Keywords: ATP; nucleotide-binding; P-loop)
F;23-219/Domain: ATP-binding motif A (P-loop)
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ABS197
ABS297
ABC transporter ATP-binding protein / ABC transporter permease protein BMEI0360 [importe C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AB3297
R;Delvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, B.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Accession: AB3297
A;Retsidues: preliminary
A;Residues: 1-381 kNRs-
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ABC transporter (ATP-binding protein) BH0281 [imported] - Bacillus halodurans (strain C-C;Species accillus halodurans
C;Species accillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: A83685
R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE008917; PIDN:AAL51541.1; PID:g17982259; GSPDB:GN00190 A;Experimental source: strain 16M C;Genetics: C;Genetics: A;Gene: BWB10360 A;Map position: I
                                                                                                                                                                                                                                                                                                                    KWPEIPQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNS 167
                                                                                                                                                                                                                                                                                                                                                                                                             R--RAKELLKUVGIBELADRRPREMSGGQQQRVAIARALANNPKILLCDEPTGNLDTKSG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KWPEIPQVLHAVGL-ESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K--RAABLINALKIGDRIDHRP-SOLSGGOOORVSIARALMWGGRIILADEFIGALDSOS 185
                                                                                                                                                                                                                                                                                           --EKH 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQL-----AVEKH 107
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                                                                                                                                                                                                                             1 MIBINDLKK-----SFGVRILMQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MIEINDLKKSF-----GVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSS
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                                                                                                                                                      17;
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                                                                                                                                                                                                                                                                                         GOILVEDVDLLKLSTRKORLYRKNTVGYLFQDYALIPDRTVKFNLQLAV---
                                                                                                     Length 226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SELVIEALRALADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 35.5%; Score 361.5; DB 2; Similarity 38.2%; Pred. No. 5.2e-24; 83; Conservative 43; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.1%; Score 358; DB 2; 39.2%; Pred. No. 2.1e-23; iive 45; Mismatches 69.
                                                      F;40-47/Region: nucleotide-binding motif A (P-loop)
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les 85; Conservative
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Best Local S:
Matches 85,
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                                                                                                     Query Match
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Mon Aug 2 09:36:56 2004

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|:| :| :| :| || || || 182 WEIIRHQNEVLGVTVILVTHDPSLAKYGDRVIRL 216

Search completed: July 27, 2004, 16:36:52 Job time: 24 secs

us-09-868-338-9.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

July 27, 2004, 16:29:29 ; Search time 13 Seconds (without alignments) 813.095 Million cell updates/sec

Run on:

US-09-868-338-9 1019 1 MIEINDLKKSFGVRILMQGL.......VVVATHSPLFRESADTIIKL 203 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	5612	311	331	123	O53899 mycobacteri		P54537 bacillus su					metha	Q9ktj5 vibrio chol	P39456 bacillus su	bacillus						O34392 bacillus su	yersinia	rickettsi	buchnera		escherich	õ	O neisseri	o,	60	75110	675 bacillus	4524
SOMMAKIES	QI		Y065 MYCGE	MACB_ECOLI	YXDL_BACSU		Y46B MYCGE	ΙZΙ	Y352 THEMA	Y46B_MYCPN	Y796 METUA	LOLD ECOLI	YFO8 METUA	METN_VIBCH	YCKI_BACSU	YXEO_BACSU	YP64_MYCTU	POTG_ECOLI	YECC_ECOLI	METN_HAEIN	FTSE ECOLI	YTRE_BACSU	METN_YERPE	Y700_RICPR	LOLD_BUCAP	LOLD_NEIMB	METN_ECOL6	METN_ECOLI	LOLD_NEIMA	ľ ľ	SA			LOLD_HAEIN
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P47705 mycoplasma	P45022 haemophilus	O9pdn2 xylella fas	P71747 mycobacteri	Q8z990 salmonella	P10346 escherichia	Q8zrm9 salmonella	Q8pc11 xanthomonas	Q82wt5 nitrosomona	Q9ck97 pasteurella	P56344 chlorella v	P07109 escherichia
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¥67 N	YA78 HAEIN	CYSA_	CYSA_N	METN	GLNO_E	METN	CYSA_	CYSA_N	METN_E	CYSA_C	HISP_E
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311	257	348	353	343	240	343	343	362	344	236	257
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27	27	27	27	27	27	27	56	56	26	56	26
r,	279	277.5	277.5	277	275.5	275	274.5	274	271	270.5	270.5
279.		.,									

ALIGNMENTS	RESULT 1 YO65_MYCPN STANDARD; PRT; 465 AA.			RN 121 RP SEQUENCE FROM N.A. RC STRAIN=ATCC 29342 / M129; RX MEDLINE=97105885; PubMed=8948633; RA Himmelleich R., Hilbert H., Plagens H., Pirkl E., Li BC.,	"Complete sequence analysis of the genome of t pneumoniae."; Nucleic Acies Res. 24:4420-4449(1996). -!- SIMILARITY: Belongs to the ABC transporter	copyright, It is produced through a utte of Bioinformatics and the EMB cs Institute. There are no restrictutions as long as its content int is not removed. Usage by and ise agreement (See http://www.isb-silse@isb-sib.ch).	DR EMBL, S73400; S73400. DR InterPro; IPR003459; AAA ATPase. DR InterPro; IPR003439; ABC_transporter. DR ProDon; P000006; ABC_transporter; 1. DR ProDon; P000006; ABC_transporter; 1. DR PROSITE; P800211; ABC_TRANSPORTER_1; 1. DR PROSITE; P850831; ABC_TRANSPORTER_2; 1. WHYPOTHETICAL PROTEIN; P3794; Transport; Complete proteome. FT NP BIND 268 273 SEQUENCE 465 AA; 53511 MW; F8F8S014C4AlA25D CRC64;	Query Match Best Local Similarity 36.7%; Pred. No. 3.18-23; Matches 77; Conservative 54; Mismatches 70; Indels 9; Gaps 4;	QY 1 MIEINDLKKSFGVRILWQGLSHKFLPGTWTALTGASGSGKSTLANCLGTLDKPSSG 56	QY 57 QILVEDVDLLKLSTRKQRLYRKUTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPE1 112
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STRAIN=K12 /
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                                        POVLHAVGLESFEEKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C., The minimal gene complement of Mycoplasma genitalium.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003593; AAA ATPASE.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_transporter.
Prodom; PD000006; ABC_transporter; 1.
PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS00211; ABC_TRANSPORTER_2; 1.
Hypothetical protein; ATP-binding; Transport; Complete proteome.
NP BIND
CONFLICT 394 399 GDEPIG - WWWTYW (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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MEDLINE=94075230; PubMed=8253680;
PEPERSON S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 466;
                                                                                                                                                                                                                                                                                                                                                                              P473<u>T1; Q49281;</u>
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter ATP-binding protein MG065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequencing.";
J. Bacteriol. 175.7918-7930(1993).
-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            466 AA; 54009 MW; A585044BBA90391C CRC64;
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                                                                                                                                                                                                                                                                                                                                                      466 AA.
                                                                                                                                                                                          411 QFLAIKQRYKTIMVIVTHNNLIAQLADLVI 440
                                                                                                                             173 ALRALADK-GATVVVATHSPLFRESADTII 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
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EMBL; U02154; AAD12436.1; -.
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les 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2097;
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      113
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61; Indels 10; Gaps

21 SHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILVEDVDLLKLSTRKQRLYRKNT 80

Conservative

Matches

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261 SHDFI-----VILGPSGSGKTTLLNIISGMDRASSGSVIVNGYNMICLNDRKLTKFRQKY 315
                                                               136
                                                                                                                                                                      Oshima T., Alba H., Baba T. Fujita K., Hayashi K., Honjo A.,
Robima T., Alba H., Baba T. Fujita K., Hayashi K., Honjo A.,
Ikemcto K., Indada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
IL PUNGTION: Efflux transporter for macrolide antibiotics. Acts in
Conjunction with macA.
Conjunction with macA.
IL SUBCELLULAR LOCATION: Integral membrane protein, Inner membrane.
C. - SUBCELLULAR LOCATION: Lothe ABC transporter family.
                                                                                     137 QORTALARVILKNPRIILADEPTGALDITNSELVIEALRALADK-GATVVVATHSPLFRE
                                                               81 VGYLFQDYALIPDRTVKFNLQLAVEKHKWP----BIPQVLHAVGLESFEEKPVFELSGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE-21429237; PubMed-11544226;
Kobayashi N., Nishino K., Yamaguchi A.;
"Novel macrolide-specific ABC-type efflux transporter in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=K12 / MG1655,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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Enterobacteriaceae, Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
MACD OR BOR99.
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Kunst R. 19044033; Funneday 3843/1, Ambulian B. W. Molecar I., Ambulian G., Azevedo V. Bertero M.G. Bessieres P., Bolotin A., Borchert S., Bacvedo V. Bertero M.G., Bessieres P., Bolotin A., Borchert S., Bacvedo V. Bertero M.G., Brans M., Braun M., Briggell S.C., Bron. S., Broullate S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., R. Broullate S., Bruschi G.V., Connerton I.F., Cummings N.J., Daniel R.A., Britz C., Eujita V., Erington J., Ferrari E., Foulger D., Achiseppi G., Guy B.U., Haga K., Haiech J., Harwood C.R., Henaut A., Ghim S.Y., Glaspel S., Hosono S., Hullo M.F., Itaya M., Jones L., Andries B., Karamata D., Hasono S., Hullo M.F., Itaya M., Jones L., Andries B., Karamata D., Kashara Y., Klaert-Blanchard M., Klein C., Robayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Ace S.M., Lavine A., Liu H., Masuda S., Hauder J., Madigue C., Medina N., Mellado R.P., Miruno M., Mostl D., Nakai S., Nobeck M., Roone D., O'Reilly M., Portetelle D., Porwollik S., Prescort A.M., Parreacan E., Pujic P., Purnelle B., Rapoport G., Ray M., Reynolds S., Rader M., Collan E., Schleich S., Schleich S., Schleich S., Schleich S., Schleich S., Schleich S., Schleich S., Schleich S., Schleich S., Soldo B., Mitters P., Wipat A., Tanaka T., Tarahashi H., Takemaru K., Malbutin S., Wallank K., Yoshikawa H., Danchin A., Tanaka T., Terpstenegger T., Minters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Willia R., Yoshikawa H., Danchin A., The Statishika R., Yoshikawa H.F., Zumstein E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wed
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R EMBL; D45912; BAA03302.1; -.

R EMBL; 299124; CAB16000.1; -.

R EMBL; 299124; CAB16000.1; -.

R D11; A70074; A70074.

R InterPro; IPR003593; AAA ATPase.

R InterPro; IPR003593; AAA ATPase.

R Pfam; PF000005; ABC transporter.

R SMART; SM00381; ABC transporter; 1.

R PROD; P500211; AAA ITANSPORTER 1; 1.

R PROSITE; P50893; ABC TRANSPORTER 2; 1.

R PROCITE; P50893; ABC TRANSPORTER 2; 1.

R PROCHELICAL Drotein; ATP-binding; Transport; Complete protecome.

T NP BIND 40 47 ATP-binding; Transport; Complete protecome.

C SEQUENCE 257 AA; 28722 MM; D9CR01E9ECCIA6AD CRC64;
                                                                    STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
              [3]
SEQUENCE FROM N.A.
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STRAIN=168 / BGSC1A1;
MEDLINE=55039891; PubMed=7952181;
Yoshida K., Sano H., Miwa Y., Ogasawara N., Fujita Y.;
"Cloning and nucleotide sequencing of a 15 kb region of the Bacillus subtilis genome containing the iol operon.";
Microbiology 140:2289-2298(1994).
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SEQUENCE FROM N.A.
STRAIN=168 / GSS01A1;
MEDIJNE=97021444; PubMed=8867804;
Yoshida K.-I., Fujimyra M., Yanai N., Fujita Y.;
Yoshida K.-I., Fujimyra M., Yanai N., Fujita Y.;
Gloning and sequencing of a 23-kb region of the Bacillus subtilis
genome between the iol and hut operons.";
DNA Res. 2:295-301(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.1%; Score 347; DB 1; Length 648; 36.9%; Pred. No. 9.4e-22; ive 42; Mismatches 81; Indels 1
R EMBL; AB071146; BAB64542.1; -
R EMBL; AB000189; AAC73966.1; -
R PIR; G64826, G64826.
R ECGGene; EG13595; macB.
R InterPro; 1PR003439; AAA_ATPase.
R InterPro; 1PR003439; ABC_transporter.
R InterPro; 1PR003439; DUF214.
R Pfan; PF00005; ABC_tran; 1.
R PF00005; Ptax; 1.
R PF00006; ABC_tran; 1.
R PF0187; SF00039; Ptax; 1.
R PF0187; SF00039; AAA, 1.
R PF0187; PS00039; AAA, 1.
R PF0187; PS00039; ABC_TRANSPORTER_1; 1.
R PROSITE; PS00039; ABC_TRANSPORTER_2; 1.
R PROSITE; PS00039; ABC_TRANSPORTER_2; 1.
R PROSITE; PS00039; ABC_TRANSPORTER_2; 1.
R PROSITE; PS00039; ABC_TRANSPORTER_2; 1.
R PROSITE; PS00039; ABC_TRANSPORTER_2; 1.
R PROSITE; PS00039; ABC_TRANSPORTER_2; 1.
R PROSITE; PS00039; ABC_TRANSPORTER_1; 1.
R PROSITE; PS00039; ABC_TRANSPORTER_2; 1.
R ATTP. Dinding; Transport; Transmembrane; POTENTIAL.
R TRANSMEM 273 293 POTENTIAL.
R TRANSMEM 576 596 POTENTIAL.
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01-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Hypothetical ABC transporter ATP-binding protein yxdl.
YXDL OR B65F OR BSU39640.
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les 79; Conservative
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437
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417
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648 AA;
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248 AA;
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                                                                                                                    16;
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                     SEQUENCE
                                                                         Query Match
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ID Y46B_MYC
AC Q92B70;
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NP BIND
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                          --LHAV----GLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSEL 169
                                                    laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the ABC transporter family. LolD subfamily.
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MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Elsen J.A., Faft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
Hypothetical protein; ATP-binding; Transport; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical ABC transporrer ATF-binding protein Rv0986/MT1014.
RV0986 OR MT1014 OR MTV044.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                          248 AA.
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InterPro; IPR001559; AAA ATPase.
InterPro; IPR001549; ABC_transporter.
Pfam; PF000005; ABC_trans, 1.
ProDom; PD000006; ABC_transporter; 1.
                                                                                                                                                                           182 VMETLQSLNRDDHVTALMVTHDPV 205
                                                                                                                                 170 VIEALRAL-ADKGATVVVATHSPL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL021999; CAA17585.1; -. EMBL; AE006985; AAK45262.1; -.
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                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                          Y986 MYCTU
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Y286 MYCTU

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 IPQ-VLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQL-----AVEKHKWPE 111
                                                                                                                                                                                                                                                                                                                                                                     56
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STRAIN-ATCC 33530 / G-37;

STRAIN-ATCC 33530 / G-37;

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STRAIN-ATCC 33530 / G-37;

Frain-Second Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-Strain-St
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MIEINDLKKSFGV----RILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSG
                                                                                                                                                                                                                                                               11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                         Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter ATP-binding protein MG468.1.
                                                                                                                                                                                                                                                               Indels
ATP (POTENTIAL).
711E0BBC872BB81A CRC64;
                                                                                                                                                                                                                                                               80;
                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 IEALRALA-DKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                            35.5%; Pred. No. 9.1e-21; ive 47; Mismatches 80
                                                                                                                                                              32.3%; Score 329.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR003593; AAA ATPase.
Interpro; IPR003493; ABC transporter.
Pfam; PP000005; ABC tran; 1.
ProDom; PD0000006; ABC_transporter; 1.
     50 A
27373 MW;
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                                                                                                                                                                                                                                                                          Conservative
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us-09-868-338-9.rsp

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129 TALRNKAVĞYIFQQYGLLRDLDVDDNIKLALPLKKRFNNNLEBLLERLELKEHRHKKVHK 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSGGEOORTALARVILKNPRIILADEPTGALDITNSELVIE-ALRALADKGATVVVATHS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunst F., Ogasawara N., Moseri I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Brans A., Braun M., Brignell S.C., Bron S., Broullet S., Bruschi C.V., Caddwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., An Denizot F., Devine K.M., Dusterfoft A., Erriarich S.D., Emmerson P.T., Brian K.D., Errington J., Pabret C., Forligt B., Calleron N., Ghims S.Y., Glaser P., Golfeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Haiech J., Harvod C.R., Henaut A., Hilbert H., Holsappel S., Esosno S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Achayashi Y., Koetter P., Koningstein G., Rugh S., Kumano M., Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Dorterelle D., Porwollik S., Prescott A.M., Parteclel D., Porwollik S., Prescott A.M., Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
                                                                                                                                                                                                                                                                                                                                                                                    14 RILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILVEDVDLLKLSTRKQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRANIE-168 / Jub642;
MAZULINE=97124195; PubWed=8869508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
Kobayashi Y.,
"Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
the Bacillus subtilis genome containing the skin element and many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 RLYRKNTVGYLFODYALIPDRTVKFNLOLA -- VEKHKWPEIPOVLHAVGLESFEEKPVFE
                                                                                                                                                                                                                                                                                                                 Gaps
SMART; SM00382, AAA; 1.

PROSITE; PS00211; ABC TRANSPORTER 1; 1.

PROSITE; PS50893; ABC_TRANSPORTER_2; 1.

Hypothetical protein; ATP-binding; Transport; Complete proteome. NP BIND 89 96

SEQUENCE 284 AA; 32256 MW; A696748EFBA43177 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable amino-acid ABC transporter ATP-binding protein yqiZ.
                                                                                                                                                                                                                                        31.9%; Score 325.5; DB 1; Length 36.3%; Pred. No. 2.3e-20; ive 44; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
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MEDLINE=98044033; PubMed=9384377;
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Microbiology 142:3103-3111(1996)
                                                                                                                                                                                                                  Query Match
Best Local Similarity 36.3%;
To, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 PLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | :||:
EKIVELAKRVIKI 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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P54537;
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-I-FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEFENDENT TRANSPORT SYSTEM FOR AN AMINO ACID. PROBABLY RESPONSIBLE FOR ENERGY COUPLIN TO THE TRANSPORT SYSTEM.

-I-SUBCELLULAR LOCATION: Membrane-associated (Potential).

-I-SIMILARITY: Belongs to the ABC transporter family. Length 240; EMBL; D84432; BAA12606.1; -.
EMBL; Z99116; CMB14327.1; -.
EMBL; Z99116; CMB14327.1; -.
Subtilist; BG1129; YGiZ.
InterPro; IPR003593; AAA_ATPase.
InterPro; DR000593; ABC_transporter.
Pfam; PF00006; ABC_tran; 1.
ProDom; PF00006; ABC_transporter; 1.
SWART; SW00382; AAA; 1.
PROSITE; PE00211; ABC_TRANSPORTER 1; 1.
PROSITE; PE00231; ABC_TRANSPORTER 2; 1.
PROSITE; PE00231; ABC_TRANSPORTER 2; 1.
PROSITE; PE00231; ABC_TRANSPORTER 2; 1. 72; Indels Y352 THEMA STANDARD; PRT; 234 AA. Q9WYĪ7; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Hypothetical ABC transporter ATP-binding protein TM0352. NP BIND 34 41 ATP (POTENTIAL). SEQUENCE 240 AA; 26949 MW; B559DA39D6C3BAAB CRC64; 61 EDVDLLKLSTRKORLYRKNTVGYLFQDYALIPDRTVKFNL----167 SELVIEALRALADKGATVVVATHSPLF-RESADTII 201 31.9%; Score 325; DB 1; 36.6%; Pred. No. 2.1e-20; tive 41; Mismatches 72; Conservative Best Local Similarity Matches 79; Conserva Thermotoga maritima Complete proteome. Query Match X352 THEMA ID Y352 THEMA ID Y352 TO DT 16-OCT. DT 15-MAR. DT HYPOTH GN TM0352 OS Thermot SOLUTION DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICIO DELLA PROPERTICIO DELLA PROPERITA PROPERTICIO DELLA PROPERTICIO DELLA PROPERTICIO DELLA PROPERT ò 셤 ઠ 셤 ò

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ch 30.7%; Score 312.5; DB 1 Similarity 37.0%; Pred. No. 2.9e-19; 71; Conservative 36; Mismatches 66
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
ABC transporter ATP-binding protein MJ0796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U34816; AAC43649.1; -.
EMBL; AE000017; AAB95805.1; -.
PIR; S62839; S62839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIVĖLAKRVIKI 261
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Methanococcus jannaschii.
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Nucleic Acids Res.
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Q58206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                  STRAIN=MSBB / DSM 3109 / ATCC 43589;
MEDLINE=9287316; PubMed=10360571;
Nelson K.B., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:123-329(1999).
Nature 399:123-329(1999).
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InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; 1.
SMART; SM00382; AAA; I.
SMART; SM00382; AAA; I.
SROSTIE; PS00211; ABC_TRANSPORTER 1; 1.
PROSTIE; PS0033; ABC_TRANSPORTER 2; 1.
Hypothetical protein; ATP-binding; Transport; Complete proteome.
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter ATP-binding protein MG468.1 homolog (ROS orf284)
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.7%; Score 323; DB 1; Length 234; 36.8%; Pred. No. 3e-20; ive 40; Mismatches 74; Indels
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Matches 71; Conservative
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                                            NCBI_TaxID=2336;
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[1]
SEQUENCE FROM N.A.
SEQUENCE 29342 / M129;
MEDLINE-80577562; PubMed-8604303;
Hilbert H., Himmelreich R., Plagens H., Herrmann R.;
"Sequence analysis of 56 kb from the genome of the bacterium
Mycoplasma pneumoniae comprising the dnaA region, the atp operon and
a cluster of ribosomal protein genes.";
Nucleic Acids Res. 24:628-639(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete sequence analysis of the genome of the bacterium Mycoplasma
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InterPro; IPR003439; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.

Pfam, PF00005; ABC_tran; I.

ProDom; PD000006; ABC transporter; I.

PROSITE; PS00211; AAA; I.

PROSITE; PS00311; ABC_TRANSPORTER 1; I.

PROSITE; PS50893; ABC_TRANSPORTER_2; I.

Hypothetical protein; ATP-binding; Transport; Complete proteome.

ATP (PDTENTIAL).

APP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 24:4420-4449(1996).
-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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121 RRK-----RALECLKMAELEERFANHKP-NQLSGGQQQRVAIARALANNPPIILADEPTG 174
KHKWPEIPQVLHAVGLESFEE----KPVFELSGGEQORTALARVLLKNPRIILADEPTG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=562;
                                                                원
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                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: :::: | :: | :: |:: :|::| : | | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | 
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8680807;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Rlake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Adams M.D., Richer G.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MIBINDLKKSF--GVRILW--QGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The crystal structure of the MJ0796 ATP-binding cassette.
Implications for the structural consequences of ATP hydrolysis in the active site of an ABC transporter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-ZAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF MUTANT GLN-171.
MEDLINE=22146558; PubMed=12150914;
Smith P.C., Karpowich N., Millen L., Moody J.E., Rosen J.,
Thomas P.J., Hunt J.F.,
"ATP binding to the motor domain from an ABC transporter drives formation of a nucleotide sandwich dimer.";
Mol. Cell 10:139-149(2002).
-! - SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probom; EUUCCE, AAA, I.
SMART; SM00382; AAA, I.
PROSITE; PS000211; ABC_TRANSPORTER_2; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
Transport; ATP-binding; Complete proteome; 3D-structure.
45 ATP (OTENTAL)
   Archaea, Buryarchaeota, Methanococci, Methanococcales, Methanocaldococcaceae, Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
MEDLINE=21402895; PubMed=11402022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR003593; AAA_ATPase.
Interpro; IPR003439; ABC_transporter.
Pfam; PP000005; ABC_tran; 1.
Probom; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 276:32313-32321(2001).
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PIR, D64399; D64399.
PDB; IFO; 25-UUL-01.
PDB; ILZT; 24-UUL-02.
TIGR; MJ0796; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 273:1058-1073(1996).
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Best Local Similarity 34.0.
Best Aca 78; Conservative
                                                                          NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  jannaschii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-11, AND CHARACTERIZATION.
MEDLINE=20245870; PubMed=10783239;
Yakushi T., Masuda K., Narita S., Matsuyama S., Tokuda H.;
Yakushi T., Masuda K., Narita S., Matsuyama S., Tokuda H.;
Yakushi T., Masuda K., Narita S., Matsuyama S., Tokuda H.;
Yakushi T., Masuda K., Narita S., Matsuyama S., Tokuda H.;
Ipiproteins from membranes...
In word In Biol. 2:212-218(2000).
In FUNCTION: Part of an ATP-dependent transport system responsible for the release of lipporceins targeted to the outer membrane for the inner membrane. Such a release is dependent of the sorting-signal (absence of an Asp at position 2 of the mature lipporcein) and of lola.
Ilpoprotein and of lola.
SUBCELLULAR LOCATION: Inner membrane-associated.
Is SINGLARITY: Belongs to the ABC transporter family. Lold subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Vanamoto Y., Vanamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-RIZ / MGGES5,
MEDLINE=97426617; Pubmed=9278503;
Blattner F.R., Flunkett G. III, Bloch C.A., Perna N.T., Burland V.
Blattner F.R., Plunkett G. III, Bloch C.A., Rayhew G.F.,
Kiley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.:
                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Bscherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
161 ALDLINSELVIEALRALADK-GATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                           LOLD ECOLI STANDARD; PRT; 233 AA.
P75557; QSR7N6;
P75557; CRE1. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 43, Last annotation update)
Lipoprotein releasing system ATP-binding protein lolD.
                        EMBL; AE000212; AAC74201.1; ALT INIT. EMBL; D90747; BAA35937.1; ALT_INIT. HSSP; Q58663; 1G6H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
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InterPro; IPR003593; AAA_ATPase.
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S FHHLLPDFTALENVAMPLLIGKKKPAEINSRALEMLKAVGLDHRANHRPSELSGGERQRV 154
                                                                                                                                                                                                                                                                                                                                                                                                        27 GTWTALTGASGSGKSTLLNCLGTLDKPSSGQILVEDVDLLKLSTRKQRLYRKNTVGYLFQ 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAINSJALS - I DSW 2661 / ATCC 43067;
MIDEJONES - STRAINSJALS - I DSW 2661 / ATCC 43067;
MIDEJONES - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAINS - STRAI
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                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-Nov-1997 (Rel. 35, Created)
01-Nov-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter ATP-binding protein MJ1508.
                                                                                                                                                                                                                             SEQUENCE 233 AA; 25438 MW; 1C305476182F1EFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.

    -!- SIMILARITY: Belongs to the ABC transporter family.

                                                                                                                                                                                                                                                                                            DB 1;
InterPro, IPR003439, ABC_transporter.

Pfam; PF00005, ABC_tran; 1.

Prodom, PD000006, ABC_transporter; 1.

SMART; SM00382; AAA; T.

PROSITE; PS00211; ABC_TRANSPORTER_1; 1.

PROSITE; PS50893; ABC_TRANSPORTER_2; 1.

ATP-binding; Transport; Complete protecome.

NP_BIND

42

49

ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                         30.4%; Score 309.5; DB 1
42.4%; Pred. No. 4.1e-19;
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                                                                                                                                                                                                                                                                                                                                            31; Mismatches
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                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42..
Local Similarity 42..
A2, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2190;
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Interpro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC transporter.
Pfam, PP000005; ABC tran; 1.
SPCODOM; PD0000006; ABC transporter; 1.
SWART; SM00382; AAA; I.

IGR; MJ1508;

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                                                                                                                                                                                                                                                                                                                                          57 QILVEDVDLLKLSTRKQRLYRKOTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKWP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                     111 EIPQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 RAKKLLEMVGLGDRLNHYPHQLSGGQQQRVAIARALANNPKIIFADEPTGNLDSKSGMAV 180
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Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Heidelberg J.F., Eisen J.A., Nelson W.C., Tettelin H., Richardson D.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.,
                                                                                                                                                                                                                                                                         1 MIEINDLKKSFG----VRILWQGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSG
                                                                                                                                                                                                                                                                                                                                                                                     EVYYKGRRISSMSENERAIFRRKISGFIFQQFHLIKTLTALENVELPMMLDERDKSYRRK
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-!- FUNCTION: Part of the binding-protein-dependent transport system maching for D-methionine. Probably responsible for energy coupling to the transport system (By similarity).

-!- SUBCELLUTAR LOCATION: Inner membrane-associated (Potential).

-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                   Gaps
PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
Hypochetical protein; Transport; ATP-binding; Complete proteome.
NP BIND 38
SEQUENCE 224 AA; 25263 MW; CF0B72742D24921E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                   10;
                                                                                                                                                   Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                 90; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable D-methionine transport ATP-binding protein metN.
                                                                                                                                                 oh 30.3%; Score 309; DB 1; Similarity 34.3%; Pred. No. 4.4e-19; 73; Conservative 40; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 MSILKGLNEKGITIIMVTHEOELTKYASKIIKL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 IEALRALADKGATVVVATHSPLFRESADTIIKL
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InterPro; IPR003439; ABC_transporter.
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STRAIN=El Tor N16961 / Serotype Ol;
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                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                       1 MIEINDLKKSFGVRILWQGLS-----HKFLP-GTMTALTGASGSGKSTLLNCLGTLD
                                                                                                                                                                                                                                                                                                                                              1 MIEIKSVNKVP-----YQGDKQIHALKDINLFIPQGTIFGVIGSSGAGKSTLIRCVNMLE
                                                                                                                                                                                                                                                                                                                                                                                           52 KPSSGQILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97124189; PubMed=8969502;
Yamane K., Kumano M., Kurita K.;
The 25 degrees-16 degrees region of the Bacillus subtilis
chromosome: determination of the sequence of a 146 kb segment and
identification of 113 genes.";
Microbiology 142:3047-3056(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIJINE=56004473; PubMed=7551042;
Rodriguez F., Grandi G.;
"An operon encoding a novel ABC-type transport system in Bacillus
                                                                                                                                                                                                                                                              22;
Pfam; PF00005; ABC_tran; 1.

Prodom; PD000006; ABC_transporter; 1.

SMART; SM0182; AAA; 1.

PROSITE; PS00211; ABC_TRANSPORTER_1; 1.

PROSITE; PS50833; ABC_TRANSPORTER_2; 1.

Transport; Amino-acid_transport; ĀTP-binding; Inner membrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable amino-acid ABC transporter ATP-binding protein yckI.
                                                                                                                                                                                                                 30.3%; Score 309; DB 1; Length 344; 36.1%; Pred. No. 7.2e-19; ive 44; Mismatches 65; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                        40D60D2C0CF52913 CRC64;
                                                                                                                                                     (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :: :: | |: : | |: 175 TTQSILELLKEINRQLNLTILLITH 199
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MEDLINE=94012481; PubMed=8407792;
                                                                                                                                                     ATP
                                                                                                                                                   NP_BIND 38 45 A.
SEQUENCE 344 AA; 37574 MW;
                                                                                                                                                                                                                                   Local Similarity 36.13
hes 74; Conservative
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C. Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.G., Connerton I.F., Cummings N.J., Daniel R.A., RA Entian K.D., Brington J.G., Connerton I.F., Cummings N.J., Daniel R.A., Entian K.D., Erington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N., RA Ginseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Hosono S., Hullo M.F., Itaya M., Jones L., RA Mirbert B., Koetter P., Koningstein G., Krogh S., Kumano M., Noris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., RA Kurita K., Lapidus A., Lurdinois S., Lauber J., Lazarevic V., RA Medina N., Mellado R.P., Mizuno M., Mosetl D., Nakai S., Noback M., Parsecan E., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M., Partelly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., RA Scriduchi J., Tamakoshi A., Tanaka T., Tarkahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Seroro E., Sinin B.S., Soldo B., Raticuchi M., Tamakoshi A., Seroro E., Vasaarotti A., Waniters P., Wipat A., Yanamoto H., Yamane K., Yasaarotti A., Waniters P., Wipat A., Yanamoto H., Yamane K., Yasaanuco K., Yata K., Waniters P., Wipat A., Yanamoto H., Yamane K., Yashaumoto R., Woshida K., Yoshikawa H.F., Zumetein B., Yoshikawa H.P., Zumetein B., Yoshikawa H.P., Zumetein B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B.,
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MEDLINE=93360913; PubMed=8355609;
MEDLINE=93360913; PubMed=8355609;
MEDLINE=93360913; PubMed=8355609;
MEDLINE=93360913; PubMed=8355609;
Wenema G., van Sinderen D.;
"Sequence and analysis of the genetic locus responsible for surfactin synthesis in Bacillus subtilis.";
Mol. Microbiol. 8:811-831(1993).
-!- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
-!- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
-!- SYSTEM FOR AN AMINO ACID. PROBABLY RESPONSIBLE FOR ENERGY COUPLING
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GOVSPV (1N REF. 2).
P -> G (1N REF. 1 AND 2).
; DO8F42F2B3490A7D CRC64;
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PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Transport; Complete proteone.
34 A1 APP BIND
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STRAIN=168 / BGSC1Al;
MEDLINE=97021444; PubMed=8867804;
Yoshida K.-I., Fujimyra M., Yanai N., Fujita Y.;
"Cloning and sequencing of a 23-kb region of the Bacillus subtilis genome between the iol and hut operons.";
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01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable amino-acid ABC transporter ATP-binding protein yxeO.
YXEO OR LP9G OR BSU39480.
Length 247;
ch 29.7%; Score 303; DB 1; Length 24 I Similarity 37.7%; Pred. No. 1.6e-18; 84; Conservative 35; Mismatches 70; Indels
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MIBINDLKKSFGVRILWQGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60
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complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                  FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR AN AMINO ACID. PROBABLY RESPONSIBLE FOR ENERGY COUPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
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                                                                                                                                                                                              TO THE TRANSPORT SYSTEM.
-!- SUBCELLULAR LOCATION: Membrane-associated (Potential).
-!- SIMILARITY: Belongs to the ABC transporter family.
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PROSITE; PS00211, ABC_TRANSPORTER 1; 1.
PROSITE; PS50893; ABC_TRANSPORTER 2; 1.
Hypothetical protein; ATP-binding; Transport; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 41 ATP (POTENTIAL).
249 AA, 27742 MW, A63886EDE69ABBOB CRC64;
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34.6%; Pred. No. 1.7e-
ive 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, D45912; BAA08331.1; -.
EMBL, Z99124; CAB15984.1; -.
PIR, A70076; A70076.
Subfilist; BG11891; yxeo.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; AAC transporter.
Pfam; PP000005; ABC transforter.
Prodom; PD000006; ABC transforter.
SWART; SM00382; AAA; I.
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Best Local Similarity 34.v..
A4, Conservative
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Run on: July 27, 2004, 16:32:35 ; Search time 38 Seconds		24 355	34.8
		m	34.8
1685.531 Million cell updates/sec			34.6
		27 352	34.5
Title: US-09-868-338-9		35	34.5
Perfect score: 1019			34.4
Sequence: 1 MISINDLKKKSFGVRILMQGLvvvvATHSPLFRESADTIIKL 203			34.4
			34.4
Scoring table: BLOSUM62		W.	34.4
Gapop 10.0 , Gapext 0.5		m	34.3
			34.2
Searched: 1017041 segs, 315518202 residues		34	34.2
			34.2
Total number of hits satisfying chosen parameters: 1017041			34.2
		38 348	34.2
Minimum DB seq length: 0			34.0
Maximum DB seq length: 2000000000			34.0
			33.9
Post-processing: Minimum Match 0%			33.9
Match	,		33.9
Listing first 45 summaries	-	34	33.8
		45 344	33.8
Database: SPTREMBL_25:*			
1: sp_archea:*			
2: sp bacteria:*			
3: sp_fungi:*			
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5: sp_invertebrate:*	RESULT	LT 1	
6: sp_mammal:*	O93ME0	E0	
7: sp_mhc:*	<u>e</u>	Q93ME0	PRELIMIN
8: sp_organelle:*	AC	Q93ME0;	
9: sp_phage:*	DT	01-DEC-2001	_
	Id	01-DEC-2001	
	TO	01-0CT-2003	3 (Trembla
	EQ.	Probable ABC transpo	3C transpo
	NG —	PCP07.	
	SO	Clostridium perfring	n perfrinç
	8	Plasmid pCP13.	P13.
	ဗ	Bacteria, Firmicutes	Firmicutes
17: sp_archeap:*) -	Clostridium	n.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

093me0 clostridium 093me0 clostridium 092th9 streptocococ 092th1 streptocococ 097ms streptocococ 097ms streptocococ 097ms streptocococ 094ms streptocococ 094ms streptocococ 094ms streptocococ 094ms streptocococ 094ms streptocococ 094ms streptocococ 094ms streptocococ 094ms streptocococ 094ms streptocococ 094ms streptocococ 094ms streptocococs 094ms streptocococs 093ms streptocococs 093ms streptocococs 093ms streptocococs 093ms streptocococs Description 093ME0 0897RU9 0892JB0 0892JB0 08DMD3 08DND2 080TA4 080TA7 080TB0 0897RB1 0897RB1 0897RB1 0897RB1 0897RB1 0897RB1 0897RB1 0897RB1 Query Match Length DB 411 408 408 406 406 399 399 386 386 380.5 380.5 380.5 375 375 371.5 Result No.

	Q831r7 shigella fl			41		Ø				Q99zf0 streptococc		Q97iv5 clostridium												Q9pm14 campylobact			past	Q8y3q9 listeria mo
028803	Q83LR7	97336	Q8YIT2	Q8RDY9	Q9L0J9	QBPOUZ	Q9KG34	029244	Q9K6Q5	Q992F0	Q81HP0	Q97IV5	Q8K7B3	Q878P3	Q9PR26	Q971X2	Q9UX77	Q8PTP8	Q8XME3	QBESM1	Q8DZX1	Q99XU3	028456	Q9PM14	Q894W5	Q88UIS	O9CNI3	Q8Y3Q9
17	16	17	16	16	16	16	16	17	16	16	16	16	16	16	16	16	17	17	16	16	16	16	17	16	16	16	16	16
226	648	232	381	224	246	233	213	228	227	233	216	232	233	237	300	255	246	265	233	250	250	224	231	217	227	664	227	207
35.5	35.4	35.3	35.1	'n.	'n.	4.	•	4.	34.6			34.4	34.4	34.4	34.4	•	34.2	34.2						33.9		ω,	33.8	33.8
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ALIGNMENTS

REQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN=13 / Type A;

WEDLINE=21664373; PubMed=11792842;

WEDLINE=21664373; PubMed=11792842;

MEDLINE=21664373; PubMed=11792842;

A Shimizu T., Ohtani K., Hirakawa H., Chshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;

A Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;

Toololete ganome sequence of Clostridium perfringens, an anaerobic R. Tesh-eater.";

Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

B MEL, AP00315; BABC445.1;

CO; GO:0046821; C:extrachromosomal DNA; IEA.

GO; GO:0046082; C:embrane; IEA.

GO; GO:004009; F:ATP-binding. IEA.

GO; GO:004009; F:ATP-binding casette (ABC) transporter acti. .; IEA.

GO; GO:004009; F:ATP-binding casette (ABC) transporter.

GO; GO:004009; F:ATP-binding. IEA.

GO; GO:006010; ABC_transporter.

InterPro; IPR003439; AAA_ATPase.

InterPro; IPR003439; AAA_ATPase.

InterPro; IPR003439; ABC_transporter.

BRART; SM00382; AAA; I.

PROSITE; PSS0893; ABC_TRANSPORTER_1; 1.

BRANT; SM0382; AAA; I.

PROSITE; PSS0893; ABC_TRANSPORTER_2; 1.

SWART; SM0382; AAA; I.

PROSITE; PSS0893; ABC_TRANSPORTER_2; 1.

PLASMid; Complete profeeone ss; Clostridia; Clostridiales; Clostridiaceae; Lrel. 19, Created)
Lrel. 19, Last sequence update)
Lrel. 25, Last annotation update)
porter. 211 AA PRT; ENARY; gens.

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63 DGDENIKINSSKSNKILREKIGYLFQNFALVDESTVYYNLHLALKYVKKNKKEKDELIKN 122 123 VLKOMNLEGYEKRKIFELSGGEQQRVSIARLLIKPSKIILADEPTGSLDAKNRDLVLYYL 182 115 VLHAVGLESFE-EKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173 61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKWPEIPQ 114 61 EDVDLIKLSTRKORLYRKNTVGYLFQDYALIPDRIVKFNLQLAV-----BKHKWPEIPQ 114 09 (ABC) transporter acti. . .; IEA 1 MIEINDLKKSFGVRILMQGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSGQILV 3 IVEOTENTITIKE FEBRILLIN FSLDIQDGELLAVTGASGSGKSTILNIIGLLEGFDSGKLIL 115 VLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEAL 6; Gaps õ Clostridium tetani. Bacteria: Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium. GOUGGERALY S.;
"The genome sequence of Clostridium tetani, the causative agent tetamus disease.";
broc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
BMBL; ARON5943; AROS5597.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004524; F:ATP binding cassette (ABC) transporter acti. GO; GO:0006810; P:ATP-binding cassette (ABC) transporter acti. GO; GO:0006810; P:ATR-binding cassette (ABC) transporter acti. InterPro; IPR003439; ABC_transporter. STRAIN-Massachusetts / E88; MEDLINE-22451253; PubMed=12552129; Brueggemann H., Bacumer S., Fricke W.F., Wiezer A., Liesegang F Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A., Gottschalk G.; Length 212; 60; Indels Complete proteome. SEQUENCE 212 AA; 23903 MW; B57A58ECBD6152EB CRC64; Created)
Last sequence update)
Last annotation update) 39.9%; Score 407; DB 16; 42.6%; Pred. No. 1.8e-25; 178 LESLKNPNRTIIIATHNPLIWEQVDQVIRV 207 212 AA 46; Mismatches 174 LRALADKGATVVVATHSPLFRESADTIIKL 203 PEGM, PE00005; ABC tran; 1.
PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.

RA HOSKINS J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., RA DeHoff B.S., Estrem S.T., Fritz L., Fu DJ., Fuller W., Geringer C., RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsuchima P., RA McAhren S.W., McHenney W., McLesster K.R., Lu J., Matsuchima P., RA Nortis F.H., O'Gara M., Perery R.B., V., Mundy C.W., Nicas T.I., RA Glass J.I.; RA Glass J.I.; RA Glass J.I.; RA Glass J.I.; RA Glass J.I.; RA Glass J.I.; REMEL, ARONG439, AAK99406.1, BR GO, GO: 0001620 / Greenbrane; IEA. DR GO, GO: 20016202 / FrAPP binding; IEA. DR GO, GO: 20016202 / FrAPP binding; IEA. DR GO, GO: 20016202 / FrAPP binding; IEA. DR GO, GO: 20016524 / FrAPP binding; IEA. DR GO, GO: 20016527 / FrAPP binding; IEA. DR GO, GO: 20016520 / FrAPP binding; IEA. DR GO, GO: 20016520 / FrAPP binding; IEA. DR GO, GO: 20016520 / FrAPP binding; IEA. DR GO, GO: 20016520 / FrAPP binding; IEA. DR GO, GO: 20016520 / FrAPP binding; IEA. DR GO, GO: 20016520 / FrAPP binding; IEA. DR GO, GO: 2001651 / FrAPP binding; IEA. DR GO, GO: 2001651 / FrAPP binding; IEA. DR GO, GO: 2001651 / FrAPP binding; IEA. DR GO, GO: 2001651 / FrAPP binding; IEA. DR GO, GO: 20016520 / FrAPP binding; IEA. DR ROSTE: PSO0353 / ABC transporter; 1. DR PROSTE: PSO0353 / ABC transporter; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 1; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 1; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 1; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 1; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 1; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 1; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 2; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 1; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 2; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 2; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 2; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 2; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 2; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 2; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 2; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 2; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 2; 1. DR PROSTE: PSO0351 / ABC TRANSPORTER 2; 1. DR PROSTE: PSO035	61 EDVDLIKLSTRKQBLYRKNTVGYLFODYALIPDRTVKFNLOLAVEKHKWPEIPO 114 i D 61 DGTSLKDIKPSVFFRDYLGYLFODYALIPDRTVKFNLOLAVGKKLKEKZENSLNKWO 117 QY 115 VLHAVGLSSFBEKDVFELGGGGCGATALARVBILLADEPTABLDFNSELLSI 177 QY 174 LALADKGPTFLEGGGEGGRAPALAKILLADPPTABLDFNSELLSI 177 QY 174 LALADKGATVVVATHSPLFRESADTIKL 203 18 ALMRVALSYLDIKQPIFELGGGEAQSVALAKILLADPPLILADEPTABLDFNSELLSI 177 QY 174 LEALADKGATVVVATHSPLFRESADTIKL 203 18 LSELKANNA PRELIMINARY, PRT; 213 AA. AC G7RNN3 PRELIMINARY, PRT; 213 AA. AC G7RNN3 PRELIMINARY, PRT; 213 AA. B C G7RNN3 AC G7RNN3 C G7RNN3 C G7RNN3 C G7RNN3 C G7RNN3 C G7RNN3 C G7RNN3 C G7RNN3 C G7RNN3 C G7RNN3 C G G G7RNN3 C G G G7RNN3 C G G G G G G G G G G G G G G G G G G
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IEA

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GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti.
GO; GO:000616; F:nuclectide binding; IEA.
GO; GO:000610; P:transport; IEA.
InterPro; IPR003593; AAA. ATPAse.
InterPro; IPR003439; ABC_transporter.
Probom; PR00005, ABC_transporter.
Probom; PR00005, ABC_transporter; I.
SMART; SM00382; AAA, I.
PROSTTE; PS00211; ABC_TRANSPORTER 1; I.
PROSTTE; PS00893; ABC_TRANSPORTER 2; I.
ATP-binding; Complete protecome.
SEQUENCE 213 AA; 23920 MW; FGBEZEA4EEB7FDB7 CRC64;
                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                        39.2%; Score 399; DB 16; Length 213; 42.9%; Pred. No. 7.9e-25; vative 40; Mismatches 70; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-00T-2001 (TrEMBLrel. 18, Created)
01-00T-2001 (TrEMBLrel. 18, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
Amino acid ABC transporter, ATP-binding protein, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
Streptococcus.
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Interpro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; 1.
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PIR; A95013; A95013.
                                                                                                                                                                                                                                                              90; Conservative
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                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDVDLLKLSTRKORLYRKNTVGYLFODYALIPDRTVKFNLQLAVEKHKWPRIPQVLHAVG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 -LESFE-----EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
                                                                                                                                                                                                                                                                                                                                                                                                                  1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MIDIQGLEKKFNDRAIFSGLNLKLEKGKVYALIGKSGSGKTTLLNILGKLEKIDGGRVLY 60
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Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoskins J., Estrem S.T., Fritz L., Full-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Kroja H., Kraft A.R., Lagace R.E.,
LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
McAbren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
                                                                                                                                                                                                                                                                                                                                                                               10; Gaps
 B.A., Morrison D.A., Hollingshead S.K., Fraser C.M., genome sequence of a virulent isolate of Streptococcus
                                                                                                                                   GO, GO:00166020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP-binding cassette (ABC) transporter acti...
GO; GO:0006610; P:TATP-binding cassette (ABC) transporter acti...
InterPro; IPR003439; ABC transporter.
Prom; PF00005; ABC transporter.
PROSITE; PS00211; ABC transporter; 1.
PROSITE; PS00211; ABC transporter; 1.
PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS0031; ABC TRANSPORTER 2; 1.
ATP-binding; Complete protecome.
SEQUENCE 213 AA; 23920 MW; F6BE2EA4EE87FDB7 CRC64;
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"Genome of the bacterium Streptococcus pneumoniae strain R6.";
"Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717 [2001].

EMBL; AE008544; AAL00604.1;
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PIR; G985232; PS5222.
PIR; G98096; G98096
G0; G0:0016020; C:membrane; IEA.
G0; G0:0005524; F:ATP binding; IEA.
                                                                                                                                                                                                                                                                                                                                             39.2%; Score 399; DB 16; Length 213; 42.9%; Pred. No. 7.9e-25; Arive 40; Mismatches 70; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter ATP-binding protein-unknown substrate.
ABC-NBD OR SPR1801.
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                     "Complete genome sequence of
                                                                    EMBL, AE007488; AAK76054.1;
PIR, E95232; E95232.
PIR, G98096; G98096.
                                    pneumoniae.";
Science 293:498-506(2001);
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nes 90; Conservative
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                                                                                                                      TIGR; SP1987;
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61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQVLHAVG 120
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GO; GO:000524; F:ATP binding; IEA.
GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
GO; GO:0000166; F:mucleotide binding; IEA.
GO; GO:0006810; P:transport; IEA.
                                                               1 MIEINDLKKSFGVRILWQGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSGQILV
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MEDLINE-21357209; PubMed=11463916;

Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,

Peterson S., Heidelberg J., Dealsen I.T., Haft D.H., Dodson R.J.,

Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

Umayam L.A., Wilte O., Salberg S.L., Lewis M.R., Radune D.,

Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,

McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey I

Holt I.E., Loftus B.J., Morrison D.A., Mollingshead S.K., Fraser C.M.;

Complete genome sequence of a virulent isolate of Streptococcus
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                                                                                                                                                                                                                                     Length 213;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-07-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter ATP-binding protein-amino acid transport.
ABC-NBD OR SPR0100.
                                                                                                                                                                                                                                                                                                        74; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Prodom, PD000006, ABC transporter; 1.
SMART; SM0382; AAA; 1.
PROSITE; PS00211, ABC TRANSPORTER 1; 1.
PROSITE; PS0939; ABC TRANSPORTER 2; 1.
ATP-binding; Complete proteome.
SEQUENCE 213 AA; 23640 MW; E3E696AEB3677399 CRC64;
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PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Complete_Troceome.
SEQUENCE 213 AA, 23626 WW; 20E696AEB367738B CRC64;
                                                                                                                                                                                                                                 37.9%; Score 386; DB 16;
40.2%; Pred. No. 9.2e-24;
tive 45; Mismatches 74;
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Best Local Similarity 40.2%
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61 FGQINLAVNSAKSQTIIREHISYLFQNFALIDDETVEYNIMLALKYVKL PKKDKLKKVEE 120
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NCBI_TaxID=1360,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TERMELrel. 15, Created)
01-0CT-2000 (TERMELrel. 15, Last sequence update)
01-0CT-2003 (TERMELrel. 25, Last annotation update)
Hypothetical ATP binding protein.
Lactococcus lactis (subsp. lactis) (Streptococcus lactis)
39.7%; Pred. No. 1.1e-23; sive 46; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 RALADKGATVVVATHSPLFRESADTIIKL 203
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33; Conservative
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Best Local Similarity 41.0
Matches 86; Conservative
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                                            83;
    Best Local
Matches 8
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Q9L650
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177 LLSLRDDNRLIIIATHNPAIWEMADEVFTM 206
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                                                                 Q8DNF2
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Q8DNF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 ALEQVGLVYLDLDKRIFELSGGESQRVALAKIILKNPPFILADEPTASIDPATSQLIMEI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO, GO.0016020; C:membrane; IEA.
GO; GO.0016020; F:ATP binding: IEA.
GO; GO.0004009; F:ATP binding sasette (ABC) transporter acti. . .; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:000377; F:DNA binding; IEA.
GO; GO:0006306; P:N-methyltransferase activity; IEA.
GO; GO:0006306; P:N-methyltransferase activity; IEA.
GO; GO:0006306; P:N-methylation; IEA.
InterPro; IPR003439; ABC transporter.
InterPro; IPR003439; ABC transporter.
InterPro; IPR003622; Ne Mtase.
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                                                                                                                                                                                                                                                                            STRAIN=ATCC BAA-34 / TIGR4;
MEDLINE=21357209; PubMed=11463916;
MEDLINE=21357209; PubMed=11463916;
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple B., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
Holt I.E., Loftus B.J., Yang F., Smith H.O., Veneer J. C.,
Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EDVDLLKLSTRKORLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEI-----PQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 210;
                                                                                                                                                                                                               Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Complete proteome,
210 AA; 23751 MW; EC0373F9E66FE167 CRC64;
                                                                                                                       01-0cT-2001 (TrEMBLrel. 18, Created)
01-0cT-2001 (TrEMBLrel. 18, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter, ATP-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.3%; Score 380.5; DB 16;
41.0%; Pred. No. 2.5e-23;
vative 41; Mismatches 72;
                                                                                                          210 AA.
            LRALADKGATVVVATHSPLFRESADTIIKL 203
                            174 LRALADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transporter; 1.
PROSITE: PS00211; ABC_TRANSPORTER 1; 1.
PROSITE: PS50893; ABC_TRANSPORTER 2; 1.
PROSITE; PS00092; NG_MTASE; 1.
                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 293:498-506(2001).
EMBL, AB007485, AAX76024.1; -.
PIR; C98093.
PIR; G95228,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 41.0%
Matches 86; Conservative
                                                                                                                                                                                                     Streptococcus pneumoniae.
                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       NCBI_TaxID=1313;
                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae.
            174
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                                                                                                       097NR1
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TIGR;
            8
                                                                                                         Db
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60 RGKD---LANYKSSDFFRHELGYLFQNFGLIENQSIEENLKLGLIGGKLSRSEQRLRQKQ 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 VLHAVGLESFE-EKPVFELSGGEOORTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
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GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0003677; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.

GO; GO:0003677; F:DN binding; IEA.

GO; GO:0000170; F:N-methyltransferase activity; IEA.

GO; GO:0000170; F:N-methyltransferase activity; IEA.

GO; GO:0000306; F:NC-methyltransferase activity; IEA.

GO; GO:0006306; F:NC-manports IEA.

InterPro; IPR003593; AAA_ATPase.

InterPro; IPR003593; AAA_ATPase.

InterPro; IPR000252; NG_Mtase.

Pfam; PF00005; ABC_transporter; 1.

Probom; PD000066; ABC_transporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDILINE-2192045; PubMed=11544234;
MEDILINE-2192045; PubMed=11544234;
MEDILINE-2192045; PubMed=11544234;
DeHoff B.S., Alborn W.E.
Gilmour R., Glass J.C., Rhoja H., Kraft A.R., Lagace R.E.,
Gilmour R., Glass J.S., Rhoja H., Kraft A.R., Lagace R.E.,
McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
Nortis F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glass J.I.;

"Genome of the bacterium Streptococcus pneumoniae strain R6.";
"Bacteriol. 183:5709-5717(2001).

EMBL, AE006141, AALO0576.1; -.

PIR; C98093; C98093.

PIR; G95228; G95228.
                                                                                                                                                                                                                                                                        Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
PROSITE; PS00925; NG_MTASE; 1.
ATP-binding; Complete proteome.
SEQUENCE 210 AA; 23751 MW; EC0373F9E6FF167 CRC64;
                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter ATP-binding protein-unknown substrate.
ABC-NBD OR SPR1773.
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=171101;
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Query Match
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Matches
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Q93H50
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Thalodurans and genomic sequence comparison with Bacillus subtilis.";
Thalodurans and genomic sequence comparison with Bacillus subtilis.";
Thalodurans and genomic sequence comparison with Bacillus subtilis.";
Thalodurans and genomic sequence comparison with Bacillus subtilis.";
Thalodurans and genomic sequence comparison with Bacillus subtilis.";
Thalodurans and genomic sequence comparison with Bacillus subtilis.";
The Back Asids Res. 284:4317-4331(2000).
The Color Control Comparison of Color Control Comparison of Color Control Comparison of Color Control Comparison of Color Control Comparison of Color Control Comparison of Color Control Comparison of Color Control Comparison of Color Control Comparison of Control Comparison of Control Comparison of Control Comparison of Control Comparison of Control Control Comparison of Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Contro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
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Bacteria; Firm.cutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBL_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
36.8%; Score 375; DB 16; Length 22
Best Local Similarity 38.1%; Pred. No. 7.9e-23;
Matches 82; Conservative 46; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS5083; ABC_TRANSPORTER_2; 1.
ATP-binding; Complete proceome.
ATP-binding; Complete proceome.
Z28 AA; Z5261 MW; E8D6912DC95BA631 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter ATP-binding protein.
                                                                                                                                                              (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                               ABC transporter (ATP-binding protein) BH3505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                       Bacillus halodurans
                                                                                                                                                                  01-OCT-2000
01-OCT-2000
01-OCT-2003
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Q9CJI3
                                    RESULT 13
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A Molotin A., Wincker P., Manger S., Jaillon O., Malarme K.,

A Meissenbach J., Ehrlich S.D., Sorokin A.;

Meissenbach J., Ehrlich S.D., Sorokin A.;

The complete genome sequence of the lactic acid bacterium Lactococcus

The complete genome sequence of the lactic acid bacterium Lactococcus

The complete genome sequence of the lactic acid bacterium Lactococcus

The complete genome sequence of the lactic acid bacterium Lactococcus

The complete genome sequence of the lactic acid bacterium Lactococcus

EMBL: ABO06240, AME04108.1;

The RBI: ABO06260; AME04108.1;

The CO: GO:000166; FATP binding cassette (ABC) transporter acti. ..; IEA.

The CO: GO:000166; Find-bending cassette (ABC) transporter acti. ..; IEA.

The CO: GO:000166; Find-bending cassette (ABC) transporter acti. ..; IEA.

The CO: GO:000166; Find-bending cassette (ABC) transporter.

The Propon; PR00349; ABC transporter.

The Propon; P000006; ABC transporter; 1.

BR SYMRT; SM00382; AAA, 11.

BR SYMRT; SM00382; AAA, 11.

BR SYMRT; SM00382; AAA, 11.
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

MEDLINE=2147403; PubMed=11572948;

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Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.;

"Genome sequence of an industrial microorganism Streptomyces avermitilis: Deducing the ability of producing secondary metabolites.";
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39.2%; Pred. No. 1.1e-22;
ive 42; Mismatches 79; Indels
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PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Complete Complete Complete Complete 201, A3, 23907 MW; A4527D636E546DCE CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
ABC transporter ATP-binding protein.
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MEDLINE=21235186; PubMed=11337471;
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SEQUENCE FROM N.A.
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

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A SAKARI Y., Hartori W., Omura S.;

**Complete genome sequence and comparative analysis of the industrial

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Sakaki Y., Hattori M., Omura S.;
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